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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:25:34 ; Search time 93.7758 Seconds
(without alignments)
7048.158 Million cell updates/sec

Title: US-10-029-436-1_COPY_61_1251
Perfect score: 1191
Sequence: 1 atgtggacagctctgcgc.....gtttccataggtccattag 1191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1191	100.0	1498	2	US-08-775-428-1
2	87.8	7.4	1382	4	US-09-364-425B-22
3	87.8	7.4	1584	1	US-08-748-485-2
4	87.8	7.4	1584	4	US-09-016-434-284
5	87	7.3	2481	1	US-08-467-568-1
6	87	7.3	2481	2	US-09-030-582-1
7	87	7.3	2481	5	PCT-US94-09051-1
8	83	7.0	1521	1	US-08-722-001-17
9	83	7.0	1567	1	US-08-722-001-24
10	83	7.0	1738	1	US-08-334-698-3
11	83	7.0	1738	1	US-08-228-932-3
12	83	7.0	1738	1	US-08-468-939-3
13	83	7.0	1738	2	US-08-406-855A-3
14	83	7.0	1738	2	US-08-722-190-3
15	83	7.0	1738	3	US-08-244-354-3
16	83	7.0	1738	3	US-09-206-899-3
17	83	7.0	1738	4	US-09-444-783-3
18	83	7.0	1738	4	US-09-688-415-3
19	83	7.0	1738	4	US-09-016-434-1402
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21	83	7.0	1738	5	PCT-US95-04203-3
22	80	6.7	1052	3	US-09-077-675A-15
23	80	6.7	1052	4	US-09-077-674-15
24	80	6.7	3129	3	US-09-077-675A-14
25	80	6.7	3129	4	US-09-077-674-14
26	78.4	6.6	1095	4	US-09-743-475-2
27	78.4	6.6	4009	4	US-09-743-475-1

28	75	6.3	1088	3	US-09-077-675A-6	Sequence 6, Appli
29	75	6.3	1088	4	US-09-077-674-6	Sequence 6, Appli
30	75	6.3	1101	4	US-09-016-434-1148	Sequence 1148, Ap
31	75	6.3	1101	4	US-09-170-496D-87	Sequence 87, Appl
32	75	6.3	1101	4	US-09-170-496D-209	Sequence 209, App
33	75	6.3	1101	4	US-09-364-425B-44	Sequence 44, Appl
34	75	6.3	1122	3	US-09-077-675A-9	Sequence 9, Appli
35	75	6.3	1122	4	US-09-077-674-9	Sequence 9, Appli
36	73.6	6.2	1050	4	US-09-762-661A-1	Sequence 1, Appli
37	70.2	5.9	7218	1	US-08-232-463-14	Sequence 14, Appl
38	70	5.9	1080	3	US-08-675-540-14	Sequence 14, Appl
39	70	5.9	1080	4	US-09-473-634-14	Sequence 14, Appl
40	69.8	5.9	1601	1	US-08-722-001-7	Sequence 7, Appli
41	69.8	5.9	1639	1	US-08-334-698-5	Sequence 5, Appli
42	69.8	5.9	1639	1	US-08-228-932-5	Sequence 5, Appli
43	69.8	5.9	1639	1	US-08-468-939-5	Sequence 5, Appli
44	69.8	5.9	1639	2	US-08-406-855A-5	Sequence 5, Appli
45	69.8	5.9	1639	2	US-08-722-190-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-775-428-1
; Sequence 1, Application US/08775428
; Patent No. 5976834
; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; APPLICANT: Fuetterer, Wendy
; APPLICANT: Bergsma, Derk
; APPLICANT: Ellis, Catherine
; TITLE OF INVENTION: CDNA CLONE HNFJL5 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,428
; FILING DATE: 09-JAN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4060
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-775-428-1

Query Match 100.0%; Score 1191; DB 2; Length 1498;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGACAGCTCTGAGCCAACTTCTCTGCTACCATGAGTCTGTGGGCTATCGT 60
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 QY 76 ATGTGGACAGCTCTGAGCCAACTTCTCTGCTACCATGAGTCTGTGGGCTATCGT 135
 Db |||||
 QY 61 TATGTTGAGTTAGTCTGGGGGTGGTGGTCTGTGACAGGACCGTGGGCAATGTGCTC 120
 Db |||||
 QY 136 TATGTTGAGTTAGTCTGGGGGTGGTGGTCTGTGACAGGACCGTGGGCAATGTGCTC 195
 Db |||||
 QY 121 ACCCTACTGGCTTGGGCTATCCAGCCCAAGCTCGTACCCGATTAACCTGCTCATAGCC 180
 Db |||||
 QY 196 ACCCTACTGGCTTGGGCTATCCAGCCCAAGCTCGTACCCGATTAACCTGCTCATAGCC 255
 Db |||||
 QY 181 AACCTCACACTGGTGTATCTCTACTGACAGCTCTCTCAGCCCTTCTCTGTGGACACC 240
 Db |||||
 QY 256 AACCTCACACTGGTGTATCTCTACTGACAGCTCTCTCAGCCCTTCTCTGTGGACACC 315
 Db |||||
 QY 241 TACCTCACACTGGTGTATCTCTACTGACAGCTCTCTCAGCCCTTCTCTGTGGACACC 300
 Db |||||
 QY 316 TACCTCACACTGGTGTATCTCTACTGACAGCTCTCTCAGCCCTTCTCTGTGGACACC 375
 Db |||||
 QY 301 TTGSCCTCCAACTTGTCTCCATCCCTGACCCCTCTGCTCATGCACTGGAGCCTACCTC 360
 Db |||||
 QY 376 TTGSCCTCCAACTTGTCTCCATCCCTGACCCCTCTGCTCATGCACTGGAGCCTACCTC 435
 Db |||||
 QY 361 CTCAATGCCCAACCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 420
 Db |||||
 QY 436 CTCAATGCCCAACCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 495
 Db |||||
 QY 421 CTGCTGAGCAGCTGGGTGTGGGGGTGGGAGCTTTGCTCCCTCTGGGCTATTTATATC 480
 Db |||||
 QY 496 CTGCTGAGCAGCTGGGTGTGGGGGTGGGAGCTTTGCTCCCTCTGGGCTATTTATATC 555
 Db |||||
 QY 481 CTGCTGAGCAGCTGGGTGTGGGGGTGGGAGCTTTGCTCCCTCTGGGCTATTTATATC 540
 Db |||||
 QY 556 CTGCTGAGCAGCTGGGTGTGGGGGTGGGAGCTTTGCTCCCTCTGGGCTATTTATATC 615
 Db |||||
 QY 541 ATCTCATGGGCTATCTTTGCTGTGGGCTCAGCAGTGTGGGCTATTTATATCCTC 600
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 QY 616 ATCTCATGGGCTATCTTTGCTGTGGGCTCAGCAGTGTGGGCTATTTATATCCTC 675
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 QY 601 ATCCACCGCCAGGTCAAAAGCAGCAGCAGCAGCAGTGGGCTATTTATATCCTC 660
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 QY 676 ATCCACCGCCAGGTCAAAAGCAGCAGCAGCAGCAGTGGGCTATTTATATCCTC 735
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 QY 661 AGCATCCATCTCAACCATGTGGCCAGGACTGATAGGCTATCTGCTGTGGTTCAGGAG 720
 Db |||||
 QY 736 AGCATCCATCTCAACCATGTGGCCAGGACTGATAGGCTATCTGCTGTGGTTCAGGAG 795
 Db |||||
 QY 721 CTGGACAGCAGGTATCATCAGAGGACCCAGTGGGCTATTTATATCCTC 780
 Db |||||
 QY 796 CTGGACAGCAGGTATCATCAGAGGACCCAGTGGGCTATTTATATCCTC 855
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 QY 781 GTTGCCACCAACCCAGACCTCGAAGGGGACTCATCAGAGTGGGAGACAGATCAACAGC 840
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 QY 841 AAGAGAGCTAAGCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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 QY 916 AAGAGAGCTAAGCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 975
 Db |||||
 QY 901 ATTAAGAGAGCAG 960
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 QY 976 ATTAAGAGAGCAG 1035
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 QY 961 TGTGTTGCTGTTGCTCTGCTTTGCTGCTGAGCTACATCCCTTCTGCTGCTCAACATT 1020
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 QY 1036 TGTGTTGCTGTTGCTCTGCTTTGCTGCTGAGCTACATCCCTTCTGCTGCTCAACATT 1095
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 QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGGTGGTCCCATGCTGTGCTGCAACCTCACCTGG 1080
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 QY 1096 CTGGATGCCAGAGTCCAGGCTCCCGGGGTGGTCCCATGCTGTGCTGCAACCTCACCTGG 1155
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QY 1081 CTCATATGGTTGATCAACCCCTGTGTCTCTATGAGCATGAACCGCAATTCGGCAAGCA 1140
 Db |||||
 QY 1156 CTCATATGGTTGATCAACCCCTGTGTCTCTATGAGCATGAACCGCAATTCGGCAAGCA 1215
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 QY 1141 TATGCTCTCATTTTAAAGAGGGGCGCGAGTTTCCATAGGCTCCATTAG 1191
 Db |||||
 QY 1216 TATGCTCTCATTTTAAAGAGGGGCGCGAGTTTCCATAGGCTCCATTAG 1266
 Db |||||

RESULT 2

US-09-364-425B-22
 ; Sequence 22, Application US/09364425B
 ; Patent No. 6653086
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; APPLICANT: Lowitz, Kevin P.
 ; APPLICANT: Chen, Ruoping
 ; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
 ; FILE REFERENCE: Aren0047
 ; CURRENT APPLICATION NUMBER: US/09/364,425B
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: 60/094,879
 ; PRIOR FILING DATE: 1998-07-31
 ; PRIOR APPLICATION NUMBER: 60/106,300
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: 60/110,906
 ; PRIOR FILING DATE: 1998-12-04
 ; PRIOR APPLICATION NUMBER: 60/121,851
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 22
 ; LENGTH: 1382
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-364-425B-22

Query Match 7.4%; Score 87.8; DB 4; Length 1382;
 Best Local Similarity 53.7%; Pred. No. 7.3e-15;
 Matches 182; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 100 GGCACCGTGGCAATGTGCTCACCTTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTACC 159
 Db |||||
 QY 181 GTCTGCTGGGAAACCTGGTGCATCGTGGTCACTTGTACAAAGAGTCTTACCTCTCACC 240
 Db |||||
 QY 160 CGATTCAACCTGTATAGCAACCTCACACTGGCTGATCTCTTACTGACGCTCTCTT 219
 Db |||||
 QY 241 CTCAGCAACAAGTTCGCTTTCAGCCTGACTCTGTCCAACCTCTCTGCTCGGTGGTG 300
 Db |||||
 QY 220 CAGCCCTTCTCTGTGGACACCTTACCTCCACCTGCGGACCGGTGCGACCTTCTGC 279
 Db |||||
 QY 301 CTGCCCTTGTGGTGTGAGAGCTCCATCCGAGGAGATGGATCTTGTGTGTGTGTGTG 360
 Db |||||
 QY 280 AGGGTATTTGGGCTCTCTCTCTTTTGGCTCAATTCCTGTCTCAATCTGACCTCTGCTC 339
 Db |||||
 QY 361 AACTTCTCTGCT 420
 Db |||||
 QY 340 ATCCGACTGGAGCTTACCT 399
 Db |||||
 QY 421 ATTGGCATCGACGCTACTATGCTGTCTGTACCCCATGTTGTACCCCATGAATCACA 480
 Db |||||
 QY 400 GCCAAGGGAGT 438
 Db |||||
 QY 481 GGGAAACCGGCTGT 519
 Db |||||

RESULT 3

US-08-748-485-2
 ; Sequence 2, Application US/08748485

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/ Patent No. 5817480
/ GENERAL INFORMATION:
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Goli, Surya K.
/ APPLICANT: Murty, Lynn E.
/ TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: US
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/748,485
/ FILING DATE: Herewith
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0159 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1584 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: Consensus
/ CLONE: 1722180
/ US-08-748-485-2
/
/ Query Match 7.4%; Score 87.8; DB 1; Length 1584;
/ Best Local Similarity 53.7%; Pred. No. 7.8e-15;
/ Matches 182; Conservative 0; Mismatches 157; Indels 0; Gaps 0
/
/ Qy 100 GGCACCGTGGCAATGTCTCACCTACTGGCCCTTGGCCATCCAGCCCAAGCTCGTACC 159
/ Db 287 GTCTGCTGGGAACCTGGTCATGGTGGTCACCTTGTACAGAAGTCTACTCCTCACC 346
/
/ Qy 160 CGATTACCTGCTCATAGCAACCTCACTGGCTGATCTCTTACTGCAAGCTCCTT 219
/ Db 347 CTCAGCAACAAGTTCGCTTCAGCCCTGACTCTGTCACACTTCTGCTGCTGTTGGT 406
/
/ Qy 220 CAGCCCTTCTCTGTGGACACCTACTCCACCTGCACTGGCGCAACGGTGCACCTTCGC 279
/ Db 407 CTGCTTTTGTGGTGACAGCTCCATCCGAGGAATGGATCTTTGGGTAGTGTGGTGC 466
/
/ Qy 280 AGGGTATTTGGGCTCCTCCTTTTTCCTCCAACTTCTGTCTCCATCCTGACCTCTGCCTC 339
/ Db 467 AACTTCTCTGGCCCTCTTACTACTGCTGATCAGCTCTGGCAGCATGCTAACCCCTCGGGGTC 526
/
/ Qy 340 ATCGCACTGGGACGGTACTCTCTCATGTGCCACCCCTAAGCTTTTTCCTCCAGTTTCAGT 399
/ Db 527 ATTGCCATCGACCGTACTATGCTCTCTGTACCCCATGGGTACCCCATGAAGATCACA 586
/
/ Qy 400 GCCAAGGGGATAGTCTGGCACTGTGTGAGCACTCGGTT 438
/ Db 587 GGGAAACCGGGCTGTATGGCACTTGTCTACATCTGGCT 625

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RESULT 4
US-09-016-434-284
; Sequence 284, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 284:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT06
; CLONE: 1722180
US-09-016-434-284

Query Match 7.4%; Score 87.8; DB 4; Length 1584;
Best Local Similarity 53.7%; Pred. No. 7,8e-15;
Matches 182; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

Qy 100 GGCACCGTGGCAATGTGCTCACCTACTGGCCTTGCCATCGACCAAGCTCGTACC 159
Db 287 GTCTGCTGGGAACCTGGTCATCGTGTGCACCTGTACAGAAGTCTACCTCTCACC 346
Qy 160 CGATTCAACCTGCTCATAGCAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTT 219
Db 347 CTACGAAACAAGTTCTGTTCTTCAGCTGACTCTGTCCAACTTCTCTGCTGTCCGTGTGGTG 406
Qy 220 CAGCCCTTCTCTGTGGACAACCTACTCCACTGTGACCTGGCCACCGGTGCCACCTCTGCG 279
Db 407 CTGCGCTTTTGTGTGACGAGCTCCATCCGAGGAATGGATCTTTGTGTGTAGTGTGGTGC 466
Qy 280 AGGGTATTGGGCTCCCTTTTGGCTCCAAATTCTGTCTCCATCTCTGACCTCTGCGCTC 339
Db 467 AACTTCTCTGCCCCTCTCTACCTGCTGATCAGCTCTGCCAGCATGCTAAACCTCGGGGTC 526
Qy 340 ATCGACTGGGAACGCTACCTCCTCATTTGGCCACCCCTAAGCTTTTTCCTCAAGTTTTCAGT 399
Db 527 ATTGGCAATGACCGCTACTATGCTGTCTGTATACCCCATGGTGTACCCCATGAAGATCACA 586

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Query Match	7.3%;	Score 87;	DB 1;	Length 2481;
Best Local Similarity	53.7%;	Pred. No. 1.6e-14;		
Matches 180;	Conservative 0;	Mismatches 155;	Indels 0;	Gaps 0;
QY	104	CGTGGGCAATGTGTACACCTACTGCGCTTGCCATCCAGCCCAAGCTCGTACCCGAT	163	
Db	225	CGTGGGAAACCTGGTCATCGTGGTCACCTTGTACAGAAGTCCCTACTCTCTCACCCCTCA	284	
QY	164	TCAACCTCTCATAGCCAACTCACCTGCGTGTATCTCTTACTGACAGCTCTCTTCAGC	223	
Db	285	GCACAAGTTCTGTCTTTCAGCGCTGACTGTGCCAACTTCTGTCTCGGTGTGGTGTGC	344	
QY	224	CCTTCTGTGTGGACACCTACTCTCACCTGCACGTGGCGCACCGGTGCCACTCTGTCAAGG	283	
Db	345	CTTTTGTGGTACGAGCTCCATCCGACAGGAATGGATCTTTGGTGTAGTGTGGTGCACCT	404	
QY	284	TATTGGGCTCCTCTCTTTTGGCTCCAAATCTGTCTTCATCTGACCCCTCTGCTCTATCG	343	
Db	405	TCTCTGCCCTCTCTACTCTGTGTATCAGCTCTGCCAGCATGTAAACCTTCGGGGTCAATTG	464	
QY	344	CACGTGGGACGCTACTCTCTCATTTGCCCAACCTTAAGCTTTTCCCCAAGTTTTTCAGTGCCA	403	
Db	465	CCATCGACCGCTACTATGCTGTCTCTGTACCCATGTGTACCCATGAAGATCAAGGGA	524	

Query Match	7.3%	Score 87;	DB 2;	Length 2481;
Best Local Similarity	53.7%;	Pred. No. 1.6e-14;		
Matches 180;	Conservative 0;	Mismatches 155;	Indels 0;	Gaps 0;
QY	104	CCGTGGGCAATGTGCTCACCTACTGGCTCTGGCCATCCAGCCAAAGCTCGTACCCGAT	163	
Db	225	CCTGGGAACCTGGTCATCGTGGTCACCTTTACAGAAATCTTACCTCTCCACCCCTCA	284	
QY	164	TCAACTTGCTCAATAGCAACACTCAACTGGCTGATCTCCTCTACTGCAACGCTCCTTCAGC	223	
Db	285	GCAACAAAGTTGCTTTCAGCCTGACTCTGTCCAACTTCTGCTGTCCGTGTGGTGTGC	344	
QY	224	CCTTCTCTGTGGACACTCACTCCACTGCTGCGCAGCCGGTGCCACTCTTGTGAGGG	283	
Db	345	CTTTTGTGTGACGAGCTCCATCCGAGGAATGATCTTTGGTGTAGTGTGGTGCAACT	404	
QY	284	TATTGGGCTCTCTCTTTTGGCTCCAAATCTGCTCCACTCCTGACCTCTGCTCATCG	343	
Db	405	TCTTGCCCTCTCTACTACCTGCTGATCAGCTCTGCCAGCATGCTAACCTCGGGGTCAATG	464	

344	CACTGGGAGCTACCTCTCATTCGCCACCTAGCTTTTCCCAAGTTTTCAGTGCCA	403
Qy		
465	CCATGACCGCTACTATGCTGCTGTACCCATGTGTACCCCATGAGATCACAGGA	524
Db		
404	AGGGGATAGTCTGGCAGCTGGTGAGCAGCTGGTT	438
Qy		
525	ACGGGCTGTGATGGCACTTGTTCATCTGGCTT	559
Db		

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Query Match	7.3%;	Score 87;	DB 5;	Length 2481;
Best Local Similarity	53.7%;	Pred. No. 1.6e-14;		
Matches 180;	Conservative	0;	Mismatches 155;	Indels 0;
Gaps	0			
QY	104	CCGTGGGCAATGTGCTCACCCCTACTCGGCGTTGGCCATCCAGCCCAAGCTCCGTACCCCGAT	163	
DB	225	CCTGGGGAAACCTGGTCATCGTGGTCACCTTGTACAAGAAAGTCTTACCTCTCTCACCCCTCA	284	
QY	164	TCAACCTGCTCATAGCCAACTCACACTGGCTGTATCTCTCTACTGCAGCTCCCTTCAGC	223	
DB	285	GCAACAAGTTGCTTTTCAGCCTGACTCTGTCCAACTTCTCTGTCGCTTTGGTGTCTGC	344	
QY	224	CCTTCTCTGTGCACACCTACCTTCCACCTGCACCTGGCGCACCGGTGCCACTTCTCGAGGG	283	
DB	345	CTTTTGTGTGCAGAGCTCCATCCGCAGGGAATGGATCTTTGGTGTAGTGTGGTGCACCT	404	
QY	284	TATTTGGGCTCTCTCTTTTGTGCTCCAAATCTGTCTCCATCTGTACCTCTCGCTCATCG	343	
DB	405	TCTCTGCCCTCTCTTACCTGTGTGATCAGCTCTGCAGCATGCTTAACCTTCGGGGTCAATG	464	
QY	344	CACCTGGGAGCGCTACCTCTCTCAITGGCCACCCCTAAAGCTTTTTTCCCAAGTTTTTCAGTGCCA	403	

Db 465 CCATCGACGGCTACTATGCTCTCTGTACCCCTGGTACCCCATGAATCACAGGA 524

Qy 404 AGGGGATAGTGTGGCACTGGTGAGCACCTGGTT 438

Db 525 ACCGGGCTGTGATGGCACTTGTACATCTGGTT 559

RESULT 8
 US-08-722-001-17
 : Sequence 17, Application US/08722001
 : Patent No. 5760054
 : GENERAL INFORMATION:
 : APPLICANT: Thompson, Wayne J.
 : APPLICANT: Huff, Joel R.
 : APPLICANT: Nerenberg, Jennie B.
 : APPLICANT: Lee, Hee-Yoon
 : APPLICANT: Bell, Ian M.
 : NUMBER OF INVENTION: ALPHA1C ADRENERGIC RECEPTOR ANTAGONISTS
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Merck & Co., Inc.
 : STREET: 126 Lincoln Avenue
 : CITY: Rahway
 : STATE: New Jersey
 : COUNTRY: United States of America
 : ZIP: 07065
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/722,001
 : FILING DATE:
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/229,276
 : FILING DATE: 14-APR-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Appollina, Mary A.
 : REGISTRATION NUMBER: 34,087
 : REFERENCE/DOCKET NUMBER: 19169Y
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (908)594-3462
 : TELEFAX: (908)594-4720
 : TELEX: 138825
 : INFORMATION FOR SEQ ID NO: 17:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 921 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: both
 : MOLECULE TYPE: cDNA
 : HYPOTHEetical: NO
 : ANTI-SENSE: NO
 US-08-722-001-17

	Query Match	7.0%	Score 83	DB 1	Length 921
	Best Local Similarity	52.1%	Pred. No. 1.4e-13		
	Matches 185	Conservative 0	Mismatches 170	Indels 0	Gaps 0
QY	100	GGCACGTTGGCAATGCTCACCTACTGSCCTTGGCCATCCAGGCCAAGCTCCGTACC	159		
DB	183	GCCATCGTGGGCAACATCTAGTCATTTGTCTGTGGCTTGCAACGGCACCTGGGACG	242		
QY	160	CGATTCAACTGCTCATAGCCAACTCACACTGGCTGATTCCTCTACTGCAAGCTCTTT	219		
DB	243	CCCACCAACTACTTTCATTTGTCACCTGGCCATGGCCGACCTGTGTTGAGCTTCACCGTC	302		
QY	220	CAGCCCTTCTCTGTGGACACCTACTCCACTGCACTGGGCGACGGGTGCCACCTTCTGC	279		
DB	303	CTGGCTTTCTCAGGGCCCTAGAGTGTCTGGTACTGGTGTCTGGGCGGGTCTTCTGTG	362		

QY 280 AGGATATTGGGCTCCTCTTTTGGCTCCAAATTCGTCTCATCTGACCCCTTGCCTC 339
 Db 363 GACATCTGGGAGCGTGGATGCTCTGCTGCACAGCGTCCATTCTGAGCTGTGGCC 422
 QY 340 ATGCGACTGGGAGCGTACTCTCTCATTCGCCACCCCTTAAGCTTTTCCCAAGTTTTCAGT 399
 Db 423 ATCTCCATCGATCGTACATCGGGGTGCGCTACTCTCTCAGTATATCCCAAGCTGTGCTACC 482
 QY 400 GCCAAGGGGATAGTCTGCGCACTGGTGAGCACTGGTTGTGGGGTGGCCAGCT 454
 Db 483 CGGAGGAAGCCATCTTGGCCCTGCTCAGTGTCTGGGCTTGTCCACCGTCACT 537

RESULT 9
 US-08-722-001-24
 ; Sequence 24, Application US/08722001
 ; Patent No. 5760054
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Wayne J.
 ; APPLICANT: Huff, Joel R.
 ; APPLICANT: Nerenberg, Jennie B.
 ; APPLICANT: Lee, Hee-Yoon
 ; APPLICANT: Bell, Ian M.
 ; TITLE OF INVENTION: ALPHA1C ADRENERGIC RECEPTOR ANTAGONISTS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merck & Co., Inc.
 ; STREET: 126 Lincoln Avenue
 ; CITY: Rahway
 ; STATE: New Jersey
 ; COUNTRY: United States of America
 ; ZIP: 07065

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/722,001
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/229,276
 FILING DATE: 14-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Appollina, Mary A.
 REGISTRATION NUMBER: 34,087
 REFERENCE/DOCKET NUMBER: 19169Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)594-3462
 TELEFAX: (908)594-4720
 TELEX: 138825

INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1567 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-722-001-24

Query Match
 Best Local Similarity 7.0%; Score 83; DB 1; Length 1567;
 Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 100 GCACCGTGGGCAATGCTGCTCACCCTACTGGCGTTGGCCATCCAGCCCAAGCTCGTACC 159
 Db 183 GCCATCGTGGGCAACATCTTGTCTGTGGCTGCAACCCGCGACCTCGGACG 242
 QY 160 CGATTCAACTGCTCATAGCAACCTCACATGGGTGATCTCTCTACTGCAAGCTCCTT 219

Db 243 CCCACCAACTACTTCAATGTCAACCTGGCCATGGCGACCTGCTGTGAGTTCAACGTC 302
 QY 220 CAGCCCTTCTGTGGACACCTACTCCACCTGCACACTGGCGACCGTGCACCTTCTGC 279
 Db 303 CTGCGCTTCTCAGCGGCGCTAGAGGTGCTCGGTACTTGGGTGCTGGGCGGATCTTCTGT 362
 QY 280 AGGATATTGGGCTCCTCTTTTGGCTCCAAATTCGTCTCATCTGACCCCTTGCCTC 339
 Db 363 GACATCTGGGAGCGCTGGATGCTCTGCTGCACAGCGTCCATTCTGAGCGTGTGGCC 422
 QY 340 ATGCGACTGGGAGCGTACTCTCTCATTCGCCACCCCTTAAGCTTTTCCCAAGTTTTCAGT 399
 Db 423 ATCTCCATCGATCGTACATCGGGGTGCGCTACTCTCTCAGTATATCCCAAGCTGTGCTACC 482
 QY 400 GCCAAGGGGATAGTCTGCGCACTGGTGAGCACTGGTTGTGGGGTGGCCAGCT 454
 Db 483 CGGAGGAAGCCATCTTGGCCCTGCTCAGTGTCTGGGCTTGTCCACCGTCACT 537

RESULT 10
 US-08-334-698-3
 ; Sequence 3, Application US/08334698
 ; Patent No. 5556753
 ; GENERAL INFORMATION:
 ; APPLICANT: Jonathan A. Bard et al.
 ; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
 ; TITLE OF INVENTION: Receptors and Uses Thereof
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOPER & DUNHAM
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10112

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/334,698
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/952,798
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 376901
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: (212) 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1738 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: N
 ANTI-SENSE: N
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 124..1683
 OTHER INFORMATION:
 US-08-334-698-3

Query Match
 Best Local Similarity 7.0%; Score 83; DB 1; Length 1738;
 Matches 52.1%; Pred. No. 1.8e-13;

Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 100 GGCACCGTGGCAATGTGCTACCTACTGGCCCTTGGCCATCAGCCCAAGCTCCGTACC 159
Db 298 GCCATCGTGGCAATGTGCTACCTACTGGCCCTTGGCCATCAGCCCAAGCTCCGTACC 357
QY 160 CGATTCAACCTGCTCATAGCCAACTCAGACTGGCTGATCTCTCTACTGCAAGCTCCTT 219
Db 358 CCCACCACTACTTCAATGTGCAACCTGGCCATGCGGCTGCTGTTGAGCTTCACCGTC 417
QY 220 CAGCCCTTCTGTGGACACCTACTCCTCATTCGACCTGGCGCACCGGTGCACCTTCTGC 279
Db 418 CTGCCCTTCTCAGCGGCGCTAGAGTCTCTGTGTCGACAGGTCATCTGAGCGCTGGCC 477
QY 280 AGGTATTTGGCTCTCTCTTTTGGCTTCCAACTGTCTCATCTGACCTGCTGCTC 339
Db 478 GACATCTGGGCGAGCGGTGATCTCTGTGTCGACAGGTCATCTGAGCGCTGGCC 537
QY 340 ATCGACTGGGACCTACTCCTCATTCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
Db 538 ATCTCCATCGATCGTACATCGGCGTGGCTACTCTCTGAGTATCCGACGCTGGTCA 597
QY 400 GCGAGGGATAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 454
Db 598 GCGAGGAAGCACTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 652

RESULT 11
US-08-932-3
; Sequence 3, Application US/08228932
; Patent No. 5578611
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
; APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
; TITLE OF INVENTION: PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,932
; FILING DATE: 13-APR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1683

; OTHER INFORMATION:
US-08-228-932-3

Query Match 7.0%; Score 83; DB 1; Length 1738;
Best Local Similarity 52.1%; Pred. No. 1.8e-13;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 100 GGCACCGTGGCAATGTGCTACCTACTGGCCCTTGGCCATCAGCCCAAGCTCCGTACC 159
Db 298 GCCATCGTGGCAATGTGCTACCTACTGGCCCTTGGCCATCAGCCCAAGCTCCGTACC 357
QY 160 CGATTCAACCTGCTCATAGCCAACTCAGACTGGCTGATCTCTCTACTGCAAGCTCCTT 219
Db 358 CCCACCACTACTTCAATGTGCAACCTGGCCATGCGGCTGCTGTTGAGCTTCACCGTC 417
QY 220 CAGCCCTTCTGTGGACACCTACTCCTCATTCGACCTGGCGCACCGGTGCACCTTCTGC 279
Db 418 CTGCCCTTCTCAGCGGCGCTAGAGTCTCTGTGTCGACAGGTCATCTGAGCGCTGGCC 477
QY 280 AGGTATTTGGCTCTCTCTTTTGGCTTCCAACTGTCTCATCTGACCTGCTGCTC 339
Db 478 GACATCTGGGCGAGCGGTGATCTCTGTGTCGACAGGTCATCTGAGCGCTGGCC 537
QY 340 ATCGACTGGGACCTACTCCTCATTCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
Db 538 ATCTCCATCGATCGTACATCGGCGTGGCTACTCTCTGAGTATCCGACGCTGGTCA 597
QY 400 GCGAGGGATAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 454
Db 598 GCGAGGAAGCACTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 652

RESULT 12

US-08-468-939-3
; Sequence 3, Application US/08468939
; Patent No. 5714381
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,939
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N

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/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 124..1683
/ OTHER INFORMATION:
/ US-08-468-939-3

Query Match
Best Local Similarity 52.1%; Pred. No. 1.8e-13;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 100 GGCACCGTGGGCAATGCTCAACCTACTGGCTTGGCCATCCAGCCCAAGTCGGTACC 159
Db 298 GCATCTGGGGCAACATCTAGTCACTTCTGTGGCTGCAACCGGCACTGGGACG 357
QY 160 CGATTCAACCTGCTCATAGCCAACTCACATGGGTGATCTCTACTGACGGTCTCTT 219
Db 358 CCACCAACTACTTCACTTCACTTGTCAACCTGGCCATGGCCGACCTGCTTCA 417
QY 220 CAGCCCTTCTGTGGACACTTCACTTCACTTGGCTGCAACCGGCACTGGCTTGC 279
Db 418 CTGCCCTTCTCAGCGCCCTAGAGTGTCTGGCTACTGGCTGCTGGGGGATCTTCT 477
QY 280 AGGGTATTGGGCTCTCTCTTTTGGCTCCAACTTCTGTCTCCATCTGACCTCTG 339
Db 478 GACATCTGGGAGCGCTGGATGCTCTGTGTCACAGCGTCCATCTGAGCGTGG 537
QY 340 ATGCACTGGGAGCGTACTCTCTCTATGCGCCACCTTAAGCTTTTCCCAAGTTTCA 399
Db 538 ATCTCCATCGATCGTACATCGGGTGGCTACTCTGCAATATCCCAAGTGGTACC 597
QY 400 GCCAAGGGATAGTGTGTCACCTGTGGACCTGGGTGTGGGGTGGCGGCTGCT 454
Db 598 CGGAGGAAGCCATCTTGGCGTGTCTGAGTGTGGGTCTTGTCCACCGTCACT 652

RESULT 13
US-08-406-855A-3
; Sequence 3, Application US/08406855A
; Patent No. 5861309
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,855A
; FILING DATE: 21-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JFW/KOB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown

/
/
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: N
/ ANTI-SENSE: N
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 124..1683
/ OTHER INFORMATION:
/ US-08-406-855A-3

Query Match
Best Local Similarity 52.1%; Pred. No. 1.8e-13;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 100 GGCACCGTGGGCAATGCTCAACCTACTGGCTTGGCCATCCAGCCCAAGTCGGTACC 159
Db 298 GCATCTGGGGCAACATCTAGTCACTTCTGTGGCTGCAACCGGCACTGGGACG 357
QY 160 CGATTCAACCTGCTCATAGCCAACTCACATGGGTGATCTCTACTGACGGTCTCTT 219
Db 358 CCACCAACTACTTCACTTCACTTGTCAACCTGGCCATGGCCGACCTGCTTCA 417
QY 220 CAGCCCTTCTGTGGACACTTCACTTCACTTGGCTGCAACCGGCACTGGCTTGC 279
Db 418 CTGCCCTTCTCAGCGCCCTAGAGTGTCTGGCTACTGGCTGCTGGGGGATCTTCT 477
QY 280 AGGGTATTGGGCTCTCTCTTTTGGCTCCAACTTCTGTCTCCATCTGACCTCTG 339
Db 478 GACATCTGGGAGCGCTGGATGCTCTGTGTCACAGCGTCCATCTGAGCGTGG 537
QY 340 ATGCACTGGGAGCGTACTCTCTCTATGCGCCACCTTAAGCTTTTCCCAAGTTTCA 399
Db 538 ATCTCCATCGATCGTACATCGGGTGGCTACTCTGCAATATCCCAAGTGGTACC 597
QY 400 GCCAAGGGATAGTGTGTCACCTGTGGACCTGGGTGTGGGGTGGCGGCTGCT 454
Db 598 CGGAGGAAGCCATCTTGGCGTGTCTGAGTGTGGGTCTTGTCCACCGTCACT 652

RESULT 14
US-08-722-190-3
; Sequence 3, Application US/08722190
; Patent No. 5990128
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George
; APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,190
; FILING DATE: 4-APR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-D-PCT/JFW/AGL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1683
; OTHER INFORMATION:
US-08-722-190-3

Query Match
Best Local Similarity 52.1%; Pred. No. 1.8e-13; Length 1738;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 100 GGCACCGTGGCAATGTGCTCACCCTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTACC 159
Db 298 GGCATCGTGGCAACATCTAGTCACTTCTGTCTGTGGCCCTGCAACCGGACCTGGGAGC 357
QY 160 CGATTCAACCTGCTCATAGCCAACTCACAATGGCTGATCTCTTACTGACGTCCTT 219
Db 358 CCCACCAACTACTTTCATTGTCAACCTGGCCATGGCCGACCTGCTGTGAGCTTCCACGTC 417
QY 220 CAGCCCTTCTGTGGACACCTACCTCCACCTGCACTGGCGCACCGGTGCCACCTCTGC 279
Db 418 CTGCCCTTCTCAGCGCCCTAGAGGTCCTGGCTACTGGGTGCTGGGCGGATCTTCTGT 477
QY 280 AGGTAATTTGGGCTCCTCCTTTTGGCTCCAAATTTGTCTCCATCCTGACCTCTGSCCTC 339
Db 538 ATCTCCATCGATCGCTACATCGGGTGCCTACTCTCTGAGTATCCACGCTGGTACC 597
QY 400 GCCAAGGGATAGTGTGGCCTGTTGGGCTGTTGGGCTGTTGGGCTGTTGGGCTGTTGGGCT 454
Db 598 CGGAGGAAGCCATCTTGGCGCTGCTCAGTGTCTGGGTCTGTGCCCGTCACTCT 652

RESULT 15
US-08-244-354-3
; Sequence 3, Application US/08244354
; Patent No. 6015819
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, et al.
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,354
; FILING DATE: April 1, 1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPW
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1683
; OTHER INFORMATION:
US-08-244-354-3

Query Match
Best Local Similarity 52.1%; Pred. No. 1.8e-13; Length 1738;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 100 GGCACCGTGGCAATGTGCTCACCCTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTACC 159
Db 298 GGCATCGTGGCAACATCTAGTCACTTCTGTCTGTGGCCCTGCAACCGGACCTGGGAGC 357
QY 160 CGATTCAACCTGCTCATAGCCAACTCACAATGGCTGATCTCTTACTGACGTCCTT 219
Db 358 CCCACCAACTACTTTCATTGTCAACCTGGCCATGGCCGACCTGCTGTGAGCTTCCACGTC 417
QY 220 CAGCCCTTCTGTGGACACCTACCTCCACCTGCACTGGCGCACCGGTGCCACCTCTGC 279
Db 418 CTGCCCTTCTCAGCGCCCTAGAGGTCCTGGCTACTGGGTGCTGGGCGGATCTTCTGT 477
QY 280 AGGTAATTTGGGCTCCTCCTTTTGGCTCCAAATTTGTCTCCATCCTGACCTCTGSCCTC 339
Db 478 GACATCTGGCAGCCGTGGATGTCCTGTGCTGCACAGCGTCCATTTCTGAGCCTGTGCGCC 537
QY 340 ATGCACTGGGACGCTACCTCTCTCATTTGCCACCTTAAGCTTTTTCCTCAAGTTTTCAGT 399
Db 538 ATCTCCATCGATCGCTACATCGGGTGCCTACTCTCTGAGTATCCACGCTGGTACC 597
QY 400 GCCAAGGGATAGTGTGGCCTGTTGGGCTGTTGGGCTGTTGGGCTGTTGGGCTGTTGGGCT 454
Db 598 CGGAGGAAGCCATCTTGGCGCTGCTCAGTGTCTGGGTCTGTGCCCGTCACTCT 652

Search completed: September 24, 2004, 04:51:48
Job time : 95.7758 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 08:34:21 : Search time 29 Seconds
(without alignments)
704.962 Million cell updates/sec

Title: US-10-029-436-2

Perfect score: 2041

Sequence: 1 MNSSDANFSCYHESVLGYR.....FRQAYGSILKGRPSFRLH 396

Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2041	100.0	396	2	US-08-775-428-2
2	293	14.4	443	1	US-07-626-618A-18
3	293	14.4	443	1	US-08-333-977-18
4	291.5	14.3	515	1	US-08-194-338-3
5	290.5	14.2	515	4	US-08-688-415-10
6	288.5	14.1	515	1	US-08-444-734A-7
7	288.5	14.1	515	2	US-08-406-855A-22
8	288.5	14.1	515	3	US-09-206-899-22
9	287.5	14.1	515	4	US-09-688-415-9
10	286.5	14.0	515	1	US-08-722-001-25
11	286.5	14.0	517	2	US-08-467-558-10
12	286.5	14.0	517	2	US-09-030-582-10
13	285.5	14.0	444	1	US-07-626-618A-19
14	285.5	14.0	444	1	US-08-333-977-19
15	285.5	14.0	520	1	US-08-334-698-4
16	285.5	14.0	520	1	US-08-228-932-4
17	285.5	14.0	520	1	US-08-468-939-4
18	285.5	14.0	520	2	US-08-406-855A-4
19	285.5	14.0	520	2	US-08-722-190-4
20	285.5	14.0	520	3	US-08-244-354-4
21	285.5	14.0	520	3	US-09-206-899-4
22	285.5	14.0	520	4	US-09-444-783-4
23	285.5	14.0	520	4	US-09-688-415-4
24	285.5	14.0	520	4	US-09-444-783-4
25	285.5	14.0	520	5	PCT-US955-04203-4
26	285	14.0	513	2	US-08-406-855A-21
27	285	14.0	513	3	US-09-206-899-21

28	283.5	13.9	444	1	US-07-781-254A-1	Sequence 1, Appl
29	281.5	13.8	466	2	US-08-406-855A-23	Sequence 23, Appl
30	281.5	13.8	466	3	US-09-206-899-23	Sequence 23, Appl
31	281.5	13.8	466	4	US-09-688-415-11	Sequence 11, Appl
32	278.5	13.6	515	3	US-09-032-742-5	Sequence 5, Appl
33	278	13.6	375	1	US-08-118-270-17	Sequence 17, Appl
34	278	13.6	375	5	PCT-US933-08528-17	Sequence 17, Appl
35	278	13.6	443	1	US-08-444-734A-3	Sequence 3, Appl
36	274.5	13.4	353	2	US-08-467-5598-10	Sequence 10, Appl
37	274	13.4	429	2	US-08-748-485-7	Sequence 7, Appl
38	274	13.4	466	1	US-08-334-698-6	Sequence 6, Appl
39	274	13.4	466	1	US-08-228-932-6	Sequence 6, Appl
40	274	13.4	466	1	US-08-468-939-6	Sequence 6, Appl
41	274	13.4	466	1	US-08-722-001-12	Sequence 12, Appl
42	274	13.4	466	1	US-08-722-001-28	Sequence 28, Appl
43	274	13.4	466	2	US-08-467-568-11	Sequence 11, Appl
44	274	13.4	466	2	US-08-406-855A-6	Sequence 6, Appl
45	274	13.4	466	2	US-08-722-190-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-775-428-2
; Sequence 2, Application US/08775428
; Patent No. 5976834
; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; APPLICANT: Fuetterer, Wendy
; APPLICANT: Bergsma, Derk
; TITLE OF INVENTION: CDNA CLONE HNFJD15 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,428
; FILING DATE: 09-JAN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4060
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-775-428-2

Query Match 100.0%; Score 2041; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.3e-176;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSVGVTGVTGNVLTLLALAIQPKLRTFNLLIA 60
 DB 1 MNSSDANFSCYHESVLGYRYVAVSVGVTGVTGNVLTLLALAIQPKLRTFNLLIA 60

QY 61 NLTADLLYCTLLQPFSDVTYHLHWRGTGATCRVFGLLFASNSVSLTCLIALGRYL 120
 DB 61 NLTADLLYCTLLQPFSDVTYHLHWRGTGATCRVFGLLFASNSVSLTCLIALGRYL 120

QY 121 LIAHPKLPQVFSKAGIVLALVSTWVGVSFAPLWPIYILVPVYCTCSFDRIRGRPYT 180
 DB 121 LIAHPKLPQVFSKAGIVLALVSTWVGVSFAPLWPIYILVPVYCTCSFDRIRGRPYT 180

QY 181 ILMGIVFVLGLSSVGFYCLIHQVRAACALDQVKLRQASHNHVARTDAMPGRFQE 240
 DB 181 ILMGIVFVLGLSSVGFYCLIHQVRAACALDQVKLRQASHNHVARTDAMPGRFQE 240

QY 241 LBSRLASGGPSEGISSEPVSAATTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 DB 241 LBSRLASGGPSEGISSEPVSAATTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300

QY 301 IKGARAPDSSBFGKVTMCFVFLCFALSTIPHLLNILDARVQAPRVHMLAANLTW 360
 DB 301 IKGARAPDSSBFGKVTMCFVFLCFALSTIPHLLNILDARVQAPRVHMLAANLTW 360

QY 361 LNCINPVLVYAMNRQFROAYGSILKRGPRSHRLH 396
 DB 361 LNCINPVLVYAMNRQFROAYGSILKRGPRSHRLH 396

RESULT 2

US-07-626-618A-18
 ; Sequence 18, Application US/07626618A
 ; Patent No. 5422265
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Tol, Hubert H.M.
 ; APPLICANT: Civelletti, Olivier
 ; TITLE OF INVENTION: A No. 5422265el Human Dopamine Receptor and Uses
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Allegretti & Witcoff, Ltd.
 ; STREET: 10 South Wacker Drive, Suite 3000
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/07/626,618A
 ; FILING DATE: 7 DEC 1990
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5422265nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 90,1092
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-715-1000
 ; TELEFAX: 312-715-1234
 ; TELEX: 810-221-8317
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 443 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; US-07-626-618A-18

Query Match 14.4%; Score 293; DB 1; Length 443;
 Best Local Similarity 25.9%; Pred. No. 2.8e-18;
 Matches 115; Conservative 66; Mismatches 179; Indels 84; Gaps 16;

QY 2 WNSDANFSCYHESVLGYRYVAVSVGVTGVTGNVLTLLALAIQPKLRTFNLLIAN 61
 DB 22 FNGSDGKADRP-----YHYVATLLTLLIAMI-VFGNVLVCMVAREKALQITNTNVLIVS 75

QY 62 LTLADLLYCTLLQPFSDVTYHLHWRGTGATCRVFGLLFASNSVSLTCLIALGRYL 119
 DB 76 LAVADLLVATLVMPWV--YLEVVGWKFSTRHCDIFVTLDMVMCTASINLCAISIDRY 133

QY 120 LLIAHPKLPQVFSKAGIVLALVSTWVGVSFAPLWPIYILVPVYCTCSFDRIRGRPYT 179
 DB 134 TAVAMPMLYNTRYSSKRRVTVMIS--IVWVLSFT-----ISCPLLFLGNADQNE 181

QY 180 TILMGIVFVLGLSSVGF-----YCLIHQ-----VKRAAQAAL----- 212
 DB 182 CIIANPAFVYSSIVSFYFVFTVLLVYIKIYVLRERRKRVNTKSSRAFAHLEAPLK 241

QY 213 -----DOYKLRQASHN-----HVARTDEAMPGRFQELD-SRLASGGPSEGISSEPV 260
 DB 242 GNCTHPEDMKLTIVKNSGSPVNRVRVDAAR--RAQLEMEMLSSTSPFETRYSPIP 299

QY 261 AATTQLEGDSSEVG-----DOINSKRAKQMAEKSPPEASAKAQPIKA 304
 DB 300 PSHHQLTLPDPSSHGLHSTPDSAPKEKNGHAKHPKIAKIFBIQTPNGKTRTS-LKTM 358

QY 305 RRAPDSSBFGKVTMCFVFLCFALSTIPHLLNILDARVQAPRVHMLAANLTW--- 361
 DB 359 SRRLSQKKEKATQMLAIVLGVFIICWLPFFFIHLINLHDCD-NIPPVLYSAFTWLGTV 417

QY 362 NGCINPVLVYAMNRQFROAYGSIL 385
 DB 418 NSAVNPIIYTTENIEFRKAFKIL 441

RESULT 3

US-08-333-977-18
 ; Sequence 18, Application US/08333977
 ; Patent No. 5594108
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Tol, Hubert H.M.
 ; APPLICANT: Civelletti, Olivier
 ; TITLE OF INVENTION: A No. 5594108el Human Dopamine Receptor and Uses
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Allegretti & Witcoff, Ltd.
 ; STREET: 10 South Wacker Drive, Suite 3000
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/333,977
 ; FILING DATE: 03-NOV-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/626,618
 ; FILING DATE: 7 DEC 1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5594108nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 90,1092
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-715-1000
 ; TELEFAX: 312-715-1234
 ; TELEX: 810-221-8317


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; TYPE: PRT
; ORGANISM: Hamster sp.
US-09-688-415-10

Query Match
  14.2%; Score 290.5; DB 4; Length 515;
  Best Local Similarity 25.1%; Pred. No. 5.7e-18;
  Matches 103; Conservative 75; Mismatches 161; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCYHE-----SVLGYYV--AVSWGVA---VTGTGCVNLTLLALAIQPKL 51
DB 17 WGEKDNFTGPNQTSNSTLPOLDVTRAIISVGLVGLGAFILFAIVGNILVILSVACNRHL 76
QY 52 RTFRNLIANLTADLLCYTLQPSVDYTLHLHWTGATFCRVFGLLFFASNSVSIITL 111
DB 77 RPTNYFIYNLAADLLSFTVLPFSATLEVGLGYVWLGRIFCDIWAADVLCCTASILSL 136
QY 112 CLIALGRYLLIAHPKLPQVFSKAGIVLAVSTWVG--VASAPL--WPIYILVPVCTC 168
DB 137 CAISIDRYIGVYSQYPTLVTRRKAILALLSVWLSTVISIGPLLGWK---EPAPND 192
QY 169 SPDRIRGRPYTILMGI-YFVLGLSSVGIFYCLIHQVKRAAQALDOYKLRQASHSNHV 227
DB 193 KECGVTEEPFYALFSSLSGSFYPLAVILVMYCRVIVAKRTTNLEAGVWKMS----- 246
QY 228 ARTDEAMPGRFQELDSRLASGGPSEGISSEPVSAATTQTLEGDSSVGDQINSKRAQMA 287
DB 247 -----NSKELTLRIHSKNPHE-----DTLSSTKAK--- 271
QY 288 EKSPPEASAKAOPKIGARRAPDSSSEFGKVTMCFVLCFALSYPILL---LNLIDAR 344
DB 272 -GNHPRSSIAVKLFKFSRE-KKAAKTLGIVGM-----FILCWDPFFIALPLGSLFST 322
QY 345 VQAPRVVHMAANLTWLCINCINPVLVYAMNROFQAYGSILKRGPRSFHR 394
DB 323 LKPPDAVKVFWLGYFNSCLNPIIYPCSSKEFKAFMRILGCQCRSGRR 372

RESULT 6
US-08-444-734A-7
; Sequence 7, Application US/08444734A
; Patent No. 5610282
; GENERAL INFORMATION:
; APPLICANT: Sibley, David R.
; APPLICANT: Mensma, Frederick J.
; APPLICANT: Mahan, Lawrence C.
; APPLICANT: McVittie, Loris D.
; TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
; receptor linked to adenylyl cyclase activation and
; expression of the receptor protein in plasmid-transfected
; cell lines
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,734A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,917
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/548,714
; FILING DATE: 06-JUL-1990

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; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH065.001FW1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-444-734A-7

Query Match
  14.1%; Score 288.5; DB 1; Length 515;
  Best Local Similarity 25.1%; Pred. No. 8.6e-18;
  Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCYHE-----SVLGYYV--AVSWGVA---VTGTGCVNLTLLALAIQPKL 51
DB 17 WGEKDNFTGPNQTSNSTLPOLDVTRAIISVGLVGLGAFILFAIVGNILVILSVACNRHL 76
QY 52 RTFRNLIANLTADLLCYTLQPSVDYTLHLHWTGATFCRVFGLLFFASNSVSIITL 111
DB 77 RPTNYFIYNLAADLLSFTVLPFSATLEVGLGYVWLGRIFCDIWAADVLCCTASILSL 136
QY 112 CLIALGRYLLIAHPKLPQVFSKAGIVLAVSTWVG--VASAPL--WPIYILVPVCTC 168
DB 137 CAISIDRYIGVYSQYPTLVTRRKAILALLSVWLSTVISIGPLLGWK---EPAPND 192
QY 169 SPDRIRGRPYTILMGI-YFVLGLSSVGIFYCLIHQVKRAAQALDOYKLRQASHSNHV 227
DB 193 KECGVTEEPFYALFSSLSGSFYPLAVILVMYCRVIVAKRTTNLEAGVWKMS----- 246
QY 228 ARTDEAMPGRFQELDSRLASGGPSEGISSEPVSAATTQTLEGDSSVGDQINSKRAQMA 287
DB 247 -----NSKELTLRIHSKNPHE-----DTLSSTKAK--- 271
QY 288 EKSPPEASAKAOPKIGARRAPDSSSEFGKVTMCFVLCFALSYPILL---LNLIDAR 344
DB 272 -GNHPRSSIAVKLFKFSRE-KKAAKTLGIVGM-----FILCWDPFFIALPLGSLFST 322
QY 345 VQAPRVVHMAANLTWLCINCINPVLVYAMNROFQAYGSILKRGPRSFHR 394
DB 323 LKPPDAVKVFWLGYFNSCLNPIIYPCSSKEFKAFMRILGCQCRSGRR 372

RESULT 7
US-08-406-855A-22
; Sequence 22, Application US/08406855A
; Patent No. 5861309
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,855A
; FILING DATE: 21-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-406-855A-22

Query Match 14.1%; Score 288.5; DB 2; Length 515;
Best Local Similarity 25.1%; Pred. No. 8.6e-18;
Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCYHE----SVLGVRVY--AVSGWVVA---VTGTGNNVLTLLALAIQPKL 51
DB 17 WGEKLDANFTGPNQTSNSTLPQLDVTRAISVGLVGLGAFILFAIVGNILVILSVACNRHL 76
QY 52 RTREFNLLIANLTADLLYCTLLQPPSVDTYHLHWRGTGATFCRVFGLLLFASNSVSLTL 111
DB 77 RTPTNYFIVNLAIAADLLSFTVLPPSATLEVILGYWVLRIFCDIWAADVLCCTASILSL 136
QY 112 CLIALGRYLLIAHPKLFPOVFSAGIVLAVSTWVG--VASFAPL--WPIYILVPVVCCTC 168
DB 137 CAISDRIVGYRYSLOYPTLVTRKAILALLSVWVLSVIGLGLGWK----EPAPND 192
QY 169 SFDRIGRPYTILMGI-YFVLGSSVGIFCLIHQVRAQAALDQYKLRQASIHSHV 227
DB 193 KECGVTEFFVALFSSLSGSFYPLAVILVMYCRVYVAKRTTKLEAGVWKMS----- 246
QY 228 ARTDEAMGRFQELDSRLASGGPSEGISSEPVSAATTQLEGDSSEVGQINSKRAKQMA 287
DB 272 -GHNPRSSIAVKLPKFSRE-KKAAKTLGIVVGM-----FILCWLPFFIALPLGSLFST 322
QY 345 VQAPRVVHMLAANLTWNGCINPVLVYAMNROFRQAYGSILKRGPRSFHR 394
DB 323 LKPPDAVPKVFVWLVGYFNCLNPPIIYPCSKFKRAFMRIILGCQCRSGRR 372

RESULT 8
US-09-206-899-22
; Sequence 22, Application US/09206899
; Patent No. 6083705
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,899
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,855
; FILING DATE: 21-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-206-899-22

Query Match 14.1%; Score 288.5; DB 3; Length 515;
Best Local Similarity 25.1%; Pred. No. 8.6e-18;
Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCYHE----SVLGVRVY--AVSGWVVA---VTGTGNNVLTLLALAIQPKL 51
DB 17 WGEKLDANFTGPNQTSNSTLPQLDVTRAISVGLVGLGAFILFAIVGNILVILSVACNRHL 76
QY 52 RTREFNLLIANLTADLLYCTLLQPPSVDTYHLHWRGTGATFCRVFGLLLFASNSVSLTL 111
DB 77 RTPTNYFIVNLAIAADLLSFTVLPPSATLEVILGYWVLRIFCDIWAADVLCCTASILSL 136
QY 112 CLIALGRYLLIAHPKLFPOVFSAGIVLAVSTWVG--VASFAPL--WPIYILVPVVCCTC 168
DB 137 CAISDRIVGYRYSLOYPTLVTRKAILALLSVWVLSVIGLGLGWK----EPAPND 192
QY 169 SFDRIGRPYTILMGI-YFVLGSSVGIFCLIHQVRAQAALDQYKLRQASIHSHV 227
DB 193 KECGVTEFFVALFSSLSGSFYPLAVILVMYCRVYVAKRTTKLEAGVWKMS----- 246
QY 228 ARTDEAMGRFQELDSRLASGGPSEGISSEPVSAATTQLEGDSSEVGQINSKRAKQMA 287
DB 247 -----NSKELTLRIHKNPHE-----DTLSSTKAK--- 271
QY 288 EKSPPEASAKAQPIKGARRAPDSSEFGKVTMCPFAVLCFALSYIPFLL---LNLIDAR 344
DB 272 -GHNPRSSIAVKLPKFSRE-KKAAKTLGIVVGM-----FILCWLPFFIALPLGSLFST 322
QY 345 VQAPRVVHMLAANLTWNGCINPVLVYAMNROFRQAYGSILKRGPRSFHR 394
DB 323 LKPPDAVPKVFVWLVGYFNCLNPPIIYPCSKFKRAFMRIILGCQCRSGRR 372

RESULT 9
US-09-688-415-9
; Sequence 9, Application US/09688415
; Patent No. 6448011
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A
; APPLICANT: Forray, Carlos
; APPLICANT: Weinshank, Richard L
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA 1 ADRENERGIC RECEPTORS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 41337aza
; CURRENT APPLICATION NUMBER: US/09/688,415
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/474,551
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 23
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APPLICATION NUMBER: US/08/467,568
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-324
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-568-10

Query Match 14.0%; Score 286.5; DB 2; Length 517;
Best Local Similarity 24.9%; Pred. No. 1.3e-17;
Matches 96; Conservative 71; Mismatches 151; Indels 67; Gaps 12;

QY 23 AVSGVVA---VTGTGVNVLTLALAIQPKLRTFNLNLTADLLYCTLLQPFSD 79
DB 45 AISVGLVGFILFAIVGNILVLSVACNRHLRTPNYFIVNLAMADLLSFTVLPFSA 104
QY 80 TYLHLWRTGATFCRVFGLLLFASNSVILTLCLALGRYLLIAHPKLPFQVFSAGIVL 139
DB 105 LEVIGYVWLGRIPCDIWAADVLCCTASILSLCAISIDRIGVYSLOYPTLVTRKAIL 164
QY 140 ALVSTWVG-VASAPL--WPIYILVPVCTCFDRIRGRPYTILMGI-YFVLGLSSVG 195
DB 165 ALLSVWLSTVISIGPLLGNK---EPAPNDKCEGVTEEPFALFSSLSGFIPLAVIL 220
QY 196 IFYCLHROVKAQAALDQYKLRQASIHNSHVARTDEAMPGRFOLDRLASGSPSGIS 255
DB 221 VMYCRVYIVAKRTTKNLEAGVWKMS-----NSKELTLRIHKNFHE--- 262
QY 256 SEPVSAAATTQLEGDSSEVGQINSKRAKMAEKSPPEASAKAOPKIGARRAPDSSEFG 315
DB 263 -----DTLSSTKAK---GHNPRSSIAVKLFKFSRE-KKAAKTLG 297
QY 316 KVTMCFVFLCFALSYIPFL---LNILDAVQAPRVVHMLAANLTWNGCINPVLVYAA 372
DB 298 IVVGM-----FILCWLFFIALPLGSLFSTLKPDPDAVKVFWLGYFNSCLNPIIYPC 350
QY 373 MNRQFQAVGSILK---RGPRSFHR 394
DB 351 SSKEFKRAFVRLGCGCGRRRRR 375

RESULT 12
US-09-030-582-10
Sequence 10, Application US/09030582
Patent No. 5994506
GENERAL INFORMATION:
APPLICANT: SOPPET, DANIEL R
TITLE OF INVENTION: ADRENERGIC RECEPTOR
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,582
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-324
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-030-582-10

Query Match 14.0%; Score 286.5; DB 2; Length 517;
Best Local Similarity 24.9%; Pred. No. 1.3e-17;
Matches 96; Conservative 71; Mismatches 151; Indels 67; Gaps 12;

QY 23 AVSGVVA---VTGTGVNVLTLALAIQPKLRTFNLNLTADLLYCTLLQPFSD 79
DB 45 AISVGLVGFILFAIVGNILVLSVACNRHLRTPNYFIVNLAMADLLSFTVLPFSA 104
QY 80 TYLHLWRTGATFCRVFGLLLFASNSVILTLCLALGRYLLIAHPKLPFQVFSAGIVL 139
DB 105 LEVIGYVWLGRIPCDIWAADVLCCTASILSLCAISIDRIGVYSLOYPTLVTRKAIL 164
QY 140 ALVSTWVG-VASAPL--WPIYILVPVCTCFDRIRGRPYTILMGI-YFVLGLSSVG 195
DB 165 ALLSVWLSTVISIGPLLGNK---EPAPNDKCEGVTEEPFALFSSLSGFIPLAVIL 220
QY 196 IFYCLHROVKAQAALDQYKLRQASIHNSHVARTDEAMPGRFOLDRLASGSPSGIS 255
DB 221 VMYCRVYIVAKRTTKNLEAGVWKMS-----NSKELTLRIHKNFHE--- 262
QY 256 SEPVSAAATTQLEGDSSEVGQINSKRAKMAEKSPPEASAKAOPKIGARRAPDSSEFG 315
DB 263 -----DTLSSTKAK---GHNPRSSIAVKLFKFSRE-KKAAKTLG 297
QY 316 KVTMCFVFLCFALSYIPFL---LNILDAVQAPRVVHMLAANLTWNGCINPVLVYAA 372
DB 298 IVVGM-----FILCWLFFIALPLGSLFSTLKPDPDAVKVFWLGYFNSCLNPIIYPC 350
QY 373 MNRQFQAVGSILK---RGPRSFHR 394
DB 351 SSKEFKRAFVRLGCGCGRRRRR 375

RESULT 13
US-07-626-618A-19
Sequence 19, Application US/07626618A
Patent No. 5422265
GENERAL INFORMATION:
APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Civeilli, Olivier
TITLE OF INVENTION: A No. 5422265el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/626,618A
; FILING DATE: 7 DEC 1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 542265nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 90,1092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 810-221-8317
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-07-626-618A-19

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Query Match 14.0%; Score 285.5; DB 1; Length 444;
Best Local Similarity 25.6%; Pred. No. 1.3e-17;
Matches 112; Conservative 70; Mismatches 185; Indels 71; Gaps 16;

QY 2 WNSDANFSCYHESVLGYRYAVGVVAVTGVGNVLTLLALAIQPKLRTFRNLLIAN 61
DB 22 FNGSEKADRP-----YNYAMLLTLFI--VFGNVLCMAVSRKALQTTNYLIVS 75
QY 62 LTLADLLYCTLOPFSVDYVHL--HWRTGATFCRVFGLLLFASNSVSLTLCIALGRY 119
DB 76 LAVADLLVATLVMPVWV--YLEVVGWKFSPRHCDFVTLDMCTASILNCAISIDRY 133
QY 120 LLIAHPKLPQVFSAGKIVLALVS--TWVGVASFAPLWPIYILVPVCTCFDRIIRGPY 178
DB 134 TAVAMPMLYNTRYSSKRRVTVMIAVWLSFTISCEL-----LFGINNTDQECIIANPA 188
QY 179 TTILMGI-----YFVLGLSSVGIFVCLIHRO-----VKRAAQAAL-----D 213
DB 189 FVYSSIVSYFVPIVTLVYIKIYIVLRKRRKRVNTKRSSAFRANKLTKLGNCTHPE 248
QY 214 QYKLRQASIHNS-----HVARTEAMPGRFOELD--SRLASGSPSEGISSEPVSAATTQT 267
DB 249 DMKLCITVIMKNSGSPVNRERMDAAR--RAQLEMEMLSSTSPPTRYSPIPPSHHQLT 306
QY 268 EGDSESVG-----DQINSKRAKQMAEKSPPEASAKAQPICKARRAPDS 310
DB 307 LPDPSSHGLHSNPDSPAKPEKNGHAKIVNPRIAKFEIQTMPNGKTRTS--LKTMSRKL 365
QY 311 SSEFGVTRMCFVAFVLCFALSYPILLNLILDAVQAPRVVHMLAANLTWL---NGCINP 367
DB 366 QQEKKATQMLAIVLGVFICHLPPFIITHLNHCDC--NIPPLYSAFTWLGYNVSNVP 424
QY 369 VLYAAMNROFRQAYGSIL 385
DB 425 ILYTTFNIEFRKAFMKIL 442

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RESULT 14
US-08-333-977-19
; Sequence 19, Application US/08333977
; Patent No. 5594108
; GENERAL INFORMATION:
; APPLICANT: Van Tol, Hubert H.M.
; APPLICANT: Civelli, Olivier
; TITLE OF INVENTION: A.No. 5594108el Human Dopamine Receptor and Uses
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Allegrretti & Witcoff, ltd.

```

```

; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,977
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/626,618
; FILING DATE: 7 DEC 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5594108nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 90,1092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 810-221-8317
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-333-977-19

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Query Match 14.0%; Score 285.5; DB 1; Length 444;
Best Local Similarity 25.6%; Pred. No. 1.3e-17;
Matches 112; Conservative 70; Mismatches 185; Indels 71; Gaps 16;

QY 2 WNSDANFSCYHESVLGYRYAVGVVAVTGVGNVLTLLALAIQPKLRTFRNLLIAN 61
DB 22 FNGSEKADRP-----YNYAMLLTLFI--VFGNVLCMAVSRKALQTTNYLIVS 75
QY 62 LTLADLLYCTLOPFSVDYVHL--HWRTGATFCRVFGLLLFASNSVSLTLCIALGRY 119
DB 76 LAVADLLVATLVMPVWV--YLEVVGWKFSPRHCDFVTLDMCTASILNCAISIDRY 133
QY 120 LLIAHPKLPQVFSAGKIVLALVS--TWVGVASFAPLWPIYILVPVCTCFDRIIRGPY 178
DB 134 TAVAMPMLYNTRYSSKRRVTVMIAVWLSFTISCEL-----LFGINNTDQECIIANPA 188
QY 179 TTILMGI-----YFVLGLSSVGIFVCLIHRO-----VKRAAQAAL-----D 213
DB 189 FVYSSIVSYFVPIVTLVYIKIYIVLRKRRKRVNTKRSSAFRANKLTKLGNCTHPE 248
QY 214 QYKLRQASIHNS-----HVARTEAMPGRFOELD--SRLASGSPSEGISSEPVSAATTQT 267
DB 249 DMKLCITVIMKNSGSPVNRERMDAAR--RAQLEMEMLSSTSPPTRYSPIPPSHHQLT 306
QY 268 EGDSESVG-----DQINSKRAKQMAEKSPPEASAKAQPICKARRAPDS 310
DB 307 LPDPSSHGLHSNPDSPAKPEKNGHAKIVNPRIAKFEIQTMPNGKTRTS--LKTMSRKL 365
QY 311 SSEFGVTRMCFVAFVLCFALSYPILLNLILDAVQAPRVVHMLAANLTWL---NGCINP 367
DB 366 QQEKKATQMLAIVLGVFICHLPPFIITHLNHCDC--NIPPLYSAFTWLGYNVSNVP 424
QY 368 VLYAAMNROFRQAYGSIL 385
DB 425 ILYTTFNIEFRKAFMKIL 442

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RESULT 15
US-08-334-698-4

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Query Match	14.0%;	Score 285.5;	DB 1;	Length 520;
Best Local Similarity	24.8%;	Pred. No. 1.6e-17;		
Matches	96;	Conservative 71;	Mismatches 151;	Indels 69; Gaps 12;
Qy	23	AVSNGVVVA--VTGTGVNLTLLALAIQPKLRTFRNLLIANLTADLLYCTLQPSVD	79	
Db	45	AISVGLVGAFLFAIVGNLIVILSVACNRHLRPTNYFIVNLAKADLLLSFTVLPSSAA	104	
Qy	80	TYLHLHWRTGATFCRFGLLILFASNSVSIITLCILIALGRYLLIAHPKLFPOVFSAGKIVL	139	
Db	105	LEVLYGVWLGRIFCDIWAADVLCCTASILSLCAISDRYIVGRYSLYQYPTLVTRRKAIL	164	
Qy	140	ALYSTVTVVG-VASFAPL--NPIYILVPVVCVTSFDRIRGRIRYVITILMGI-YFVLGLSSVG	195	
Db	165	ALLSVWLSTVISLGPLGWK-----EAPNDKCGVTEEPFYALFSLSGSYFPLAVIL	220	
Qy	196	IFYCLIHROVKRAAQALDQYKLRQASIHNSNHVARTDEAMPGRFOELPSRLASGGPSEGIS	255	
Db	221	VMYCRVIVAKRTTKNLEAGVNMKMS-----NSKELTLRIHSKNFHE---	262	
Qy	256	SEPVSAATTQTLEGDSSEVGDOIINSKRAQVAEKSPPPEASAKAOPIKGARAPDSSSEFG	315	
Db	263	-----DTLSTRAK-----GHNPRSSIIVKLFKFSRE-KKAAKTGLG	297	
Qy	316	KVTRMCFVFLCFAISLYIFPLL---LNLILDVAQVPRVVHMLAANLTWNGCINPVLVAA	372	
Db	298	IIVGM-----FILCWLPFIALLGLSLFTLKPDPDAVFKVFWLGVFNSLAPIIYPC	350	
Qy	373	MNRFRQAYGSIL-----KRGPRSFHR	394	
Db	351	SSKEFKFAFVRIILGCQCRGRGRRRRR	377	

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:25:34 ; Search time 103.224 Seconds
(without alignments)
7048.158 Million cell updates/sec

Title: US-10-029-436-1

Perfect score: 1311

Sequence: 1 ttgaatgctaggtcttctgatt.....caggaccacaaagtgcaggta 1311

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/prodata/2/ina/5B COMB seq:
3: /cgn2_6/prodata/2/ina/5A COMB seq:
4: /cgn2_6/prodata/2/ina/5B COMB seq:
5: /cgn2_6/prodata/2/ina/PCTUS COMB seq:
6: /cgn2_6/prodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	87.8	6.7	1382	4	US-09-364-425B-22
3	87.8	6.7	1584	1	US-08-748-485-2
4	87.8	6.7	1584	4	US-09-016-434-284
5	87	6.6	2481	1	US-08-467-568-1
6	87	6.6	2481	2	US-09-030-582-1
7	87	6.6	2481	5	PCT-US94-09051-1
8	83	6.3	921	1	US-08-722-001-17
9	83	6.3	1567	1	US-08-722-001-24
10	83	6.3	1738	1	US-08-334-698-3
11	83	6.3	1738	1	US-08-228-932-3
12	83	6.3	1738	1	US-08-468-939-3
13	83	6.3	1738	2	US-08-406-855A-3
14	83	6.3	1738	2	US-08-722-190-3
15	83	6.3	1738	3	US-08-244-354-3
16	83	6.3	1738	3	US-09-806-899-3
17	83	6.3	1738	3	US-08-444-782-3
18	83	6.3	1738	4	US-09-688-415-3
19	83	6.3	1738	4	US-09-016-434-1402
20	83	6.3	1738	4	US-09-444-783-3
21	83	6.3	1738	5	PCT-US95-04203-3
22	80	6.1	1092	3	US-09-077-675A-15
23	80	6.1	1092	4	US-09-077-674-15
24	80	6.1	3129	3	US-09-077-675A-14
25	80	6.1	3129	4	US-08-077-674-14
26	78.4	6.0	1095	2	US-09-743-475-2
27	78.4	6.0	4009	4	US-09-743-475-1

28	75	5.7	1088	3	US-09-077-675A-6	Sequence 6, Appli
29	75	5.7	1088	4	US-09-077-674-6	Sequence 6, Appli
30	75	5.7	1101	4	US-09-016-434-1148	Sequence 1148, Ap
31	75	5.7	1101	4	US-09-170-496D-87	Sequence 87, Appl
32	75	5.7	1101	4	US-09-170-496D-209	Sequence 209, App
33	75	5.7	1101	4	US-09-364-425B-44	Sequence 44, Appl
34	75	5.7	1122	3	US-09-077-675A-9	Sequence 9, Appli
35	75	5.7	1122	4	US-09-077-674-9	Sequence 9, Appli
36	73.6	5.6	1050	4	US-09-762-661A-1	Sequence 1, Appli
37	70.2	5.4	7218	1	US-08-232-463-14	Sequence 14, Appl
38	70	5.3	1080	3	US-08-875-540-14	Sequence 14, Appl
39	70	5.3	1080	4	US-09-473-634-14	Sequence 14, Appl
40	69.8	5.3	1601	1	US-08-722-001-7	Sequence 7, Appli
41	69.8	5.3	1639	1	US-08-334-698-5	Sequence 5, Appli
42	69.8	5.3	1639	1	US-08-228-932-5	Sequence 5, Appli
43	69.8	5.3	1639	1	US-08-468-939-5	Sequence 5, Appli
44	69.8	5.3	1639	2	US-08-406-855A-5	Sequence 5, Appli
45	69.8	5.3	1639	2	US-08-722-190-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-775-428-1
; Sequence 1, Application US/08775428
; Patent No. 5978834
; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; APPLICANT: Fuetterer, Wendy
; APPLICANT: Bergsma, Derk
; APPLICANT: Ellis, Catherine
; TITLE OF INVENTION: CDNA CLONE HNEJD15 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,428
FILING DATE: 09-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50042
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4060
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1498 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-775-428-1
Query Match 95.8%; Score 1256.4; DB 2; Length 1498;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 TTAGCTCTATCATGTGGAACAGCTCTGAGCCAACTTCTCTGCTACCATGAGTCTGTG 108

DB 64 TCAGCCTCTATCATGTGGAACAGCTCTGAGCCAACTTCTCTGCTACCATGAGTCTGTG 123

QY 109 CTGGCTATCTGTTATGTGAGTGTAGCTGGGGGTGTGTGGTGTGAGCAGGACCGTG 168

DB 124 CTGGCTATCTGTTATGTGAGTGTAGCTGGGGGTGTGTGGTGTGAGCAGGACCGTG 183

QY 169 GGCAATGTGTCAACCTTACTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAC 228

DB 184 GGCAATGTGTCAACCTTACTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAC 243

QY 229 CTGCTCATAGCAACCTCACACTGGCTGATCTCTCTACTGACGCTCTCTACGCCCTTC 288

DB 244 CTGCTCATAGCAACCTCACACTGGCTGATCTCTCTACTGACGCTCTCTACGCCCTTC 303

QY 289 TCTGTGACACCTTACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGAGGGTATTT 348

DB 304 TCTGTGACACCTTACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGAGGGTATTT 363

QY 349 GGCTCTCTCTTTTGTGCTCAATCTGTCTCATCTGCACTGCTGCTGCTGCTGCTGCTG 408

DB 364 GGCTCTCTCTTTTGTGCTCAATCTGTCTCATCTGCACTGCTGCTGCTGCTGCTGCTG 423

QY 409 GAGCGTACTCTCTATGTCACCTTCCACCTTAACTTTTCCCAAGTTTTCAGTCCAGGGG 468

DB 424 GAGCGTACTCTCTATGTCACCTTCCACCTTAACTTTTCCCAAGTTTTCAGTCCAGGGG 483

QY 469 ATAGTGTGCACTGTGAGCACTGCTGGGTGTGGCGTGGCCAGTTTCTGCTCCCTCTGG 528

DB 484 ATAGTGTGCACTGTGAGCACTGCTGGGTGTGGCGTGGCCAGTTTCTGCTCCCTCTGG 543

QY 529 CCTATTATATCTGTACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588

DB 544 CCTATTATATCTGTACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603

QY 589 CCTTACACCACTCTCTATGTCACCTTCCACCTTAACTTTTCCCAAGTTTTCAGTCCAG 648

DB 604 CCTTACACCACTCTCTATGTCACCTTCCACCTTAACTTTTCCCAAGTTTTCAGTCCAG 663

QY 649 TTCTATTGCTCTATCCACCGCAGTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708

DB 664 TTCTATTGCTCTATCCACCGCAGTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723

QY 709 TTGCGACAGGCAAGCATCCACTCCAACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768

DB 724 TTGCGACAGGCAAGCATCCACTCCAACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783

QY 769 CTTTTCAGGAGCTGGAAGAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCT 828

DB 784 CTTTTCAGGAGCTGGAAGAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCT 843

QY 829 GAGCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888

DB 844 GAGCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903

QY 889 CAGATCAACAGAGAGCTAAGCAGATGTCAGAGAAAGCCCTCCAGAGCATCTGCC 948

DB 904 CAGATCAACAGAGAGCTAAGCAGATGTCAGAGAAAGCCCTCCAGAGCATCTGCC 963

QY 949 AAAGCCAGGCAATTAAGAGGACGAGAGCTGCGGATTTTCATCGGAATTTGGAAG 1008

DB 964 AAAGCCAGGCAATTAAGAGGACGAGAGCTGCGGATTTTCATCGGAATTTGGAAG 1023

QY 1009 GTGACTCGAATGTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068

DB 1024 GTGACTCGAATGTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1083

QY 1069 CTGCTCAACATCTGGATGTCAGAGTCCAGCTCCCGGGTGTGTCATGCTGCTGCC 1128

DB 1084 CTGCTCAACATCTGGATGTCAGAGTCCAGCTCCCGGGTGTGTCATGCTGCTGCC 1143

QY 1129 AACCTCACCTGCTCAATGGTTGATCAACCTTGTGCTCTATGAGCCATGAACCGCCAA 1188

DB 1144 AACCTCACCTGCTCAATGGTTGATCAACCTTGTGCTCTATGAGCCATGAACCGCCAA 1203

QY 1189 TTCCGCCCAAGCATATGGCTCCATTTTAAAGAGGGGCCCCGGAGTTTCCATAGGCTCCAT 1248

DB 1204 TTCCGCCCAAGCATATGGCTCCATTTTAAAGAGGGGCCCCGGAGTTTCCATAGGCTCCAT 1263

QY 1249 TAGACTGTGACCTTAGTCACAGAAATTCAGAGTGTCTCTCCAGACCAAAAGTGGC 1306

DB 1284 TAGACTGTGACCTTAGTCACAGAAATTCAGAGTGTCTCTCTCCAGACCAAAAGTGGC 1321

RESULT 2

US-09-364-425B-22
 ; Sequence 22, Application US/09364425B
 ; Patent No. 665386
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; APPLICANT: Lowitz, Kevin P.
 ; APPLICANT: Chen, Ruoping
 ; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
 ; FILE REFERENCE: Azen0047
 ; CURRENT APPLICATION NUMBER: US/09/364,425B
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: 60/094,879
 ; PRIOR FILING DATE: 1998-07-31
 ; PRIOR APPLICATION NUMBER: 60/106,300
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: 60/110,906
 ; PRIOR FILING DATE: 1998-12-04
 ; PRIOR APPLICATION NUMBER: 60/121,851
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 22
 ; LENGTH: 1382
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-364-425B-22

Query Match 6.7%; Score 87.8; DB 4; Length 1382;

Best Local Similarity 53.7%; Pred. No. 1.2e-15;
 Matches 182; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 160 GGACCGTGGCAATGTGCTCACCTTACCTGGCTTGGCCATCCAGCCCAAGCTCCGTACC 219

DB 181 GTCTGCTGGGAAACCTGTGCTATCTGTGTCACCTTGTACAGAGTCTTACCTCTCACC 240

QY 220 CGATTCAACCTGCTCATAGCCAACTCAGCTGGGTGATCTCTCTACTGACGCTCCTT 279

DB 241 CTGAGCAACAGTGTGCTTTCAGCCTGACTCTGTCCAACTTCTCTGCTGCTGGTGTG 300

QY 280 CAGCCCTTCTCTGTGGAGACCTTACCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 339

DB 301 CTGCTTTTGTGGTGGAGAGTCTTCCAGAGTCTTCCAGAGGATGGATCTTTGGTGTAGTGGTGC 360

QY 340 AGGATTATTGGGCTCCTCTTTTGGCTCCCAATTTGTCTGCTCCTCCTCCTCCTCCTCCTC 399

DB 361 AACTTCTCTGCCCTCCTCTTACCTGCTGATGAGTCTGCGCAGATGCTAACCTCGGGTC 420

QY 400 ATCGCACTGGGACGCTACTCTCTCATGCGCCACCTTAAGCTTTTCCCAAGTTTTCAGT 459

DB 421 ATGGCACTGGACCGCTACTATGCTGTCTGTACCCCATGGTGTACCCCATGAAGATCACA 480

QY 460 GCCAAGGGGATGCTGGCACTGGTGGACCTGGGTT 498

DB 481 GGGACCGGCTGTGATGGCACTTGTCTACATCTGGCTT 519

460 GCCACAGGGGATAGTCTCGCACTGTGTAGCACCTGGGTT 498
DB |||||
587 GGGAAACGGGCTGTGATGCCACTTGTTCACATCTGGCTT 625

RESULT 4
US-09-016-434-284
; Sequence 284, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; Zip: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 284:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1594 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT06
; CLONE: 1722180
; US-09-016-434-284

	Query Match	6.7%;	Score 87.8;	DB 4;	Length 1584;
	Best Local Similarity	53.7%;	Prod. No. 1.3e-15;		
	Matches 182;	Conservative 0;	Mismatches 157;	Indels 0;	Gaps 0;
160	QY	GGCAACCTGGCGAATGTGTCTACCTCTATGGCGCTTGGCCATCCAGCCCAAGCTCGTACC	219		
287	Db	GTCTGCTGGGAACCTGTGTATCGGGFCACCTTGTACAAAGATCTACTCTCTCACC	346		
220	QY	CGATTCAACCTGTCTATAGCCAACTCACTACCTGGCTGATCTCCTCTACTGCACGCTCCTT	279		
347	Db	CTCAGCAACAAGTTCGTCTCTCAGCTCGACTCTGTCCAACTTCTCTGCTCTCGCTGTGGTG	406		
280	QY	CAGCCCTTCTCTGGACACCTACCTCTCACTTGCATCGCGCACCGGTGCCACCTTCTGC	339		
407	Db	CTGCCTTTTGTGTGACGAGCTCCATCCACGGGAATGGATCTTTGGTGTAGTGTGGTGC	466		
340	QY	AGGGTATTGGGGTCTCTCTTTTGGCTCCAAATCTGTCTCCATCTCGACCTCTGCCTC	399		
467	Db	AACCTTCTCGCTCTCTACTGTCTGATCAGCTCTGCCAGCATGCTAAACCTCGGGGTC	526		

QY 400 ATCCAGTGGAGCGTACCTCTCTATGCCCCACCCAGCTTTTCCCAAGTTTTCAGT 459
Db 527 ATTGGCATCCAGCGTACTATGCTGCTGTACCCCATGGTGACCCCATGAAGATCACA 586
QY 460 GCCAAGGGGATAGTGTGGCACTGGTGAGCACTGGGTT 498
Db 587 GGGAAACGGGCTGTGATGGCACTTGTCTACATCTGGCTT 625

RESULT 5

US-08-467-568-1
; Sequence 1, Application US/08467568
; Patent No. 5817477
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,568
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-324
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101...1687
US-08-467-568-1

Query Match 6.6%; Score 87; DB 1; Length 2481;
Best Local Similarity 53.7%; Pred. No. 2.8e-15;
Matches 180; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 164 CCGTGGGCAATGTCTACCTACTGGCGCTTGGCCATCCAGCCCAAGCTCCGTACCCGAT 223
Db 225 CCGTGGGCAATGTCTACCTACTGGCGCTTGGCCATCCAGCCCAAGCTCCGTACCCGAT 284
QY 224 TCAACCTGCTCATAGCCAACTCAGTGGGTGATCTCTCTACTGACGCTCCCTTCAGC 283
Db 285 GCAACAAGTTCGTCTTACGCTGACTCTGTCCAACTTCTCTGCTGTGGTGTGGTGTGC 344
QY 284 CTTTCTGTGGACACCTTACCTCAGCTGCTGCGGCGACGGTGCCACCTTCTGAGGG 343
Db 345 CTTTGTGGTGACAGCTTCAATCCGCGAGGGAATGGATCTTTGGTGTAGTGTGGTCAACT 404
QY 344 TATTGGGCTCCTCTCTTTTGGCTTCCAAATCTGTCTCCATCTGACCTCTGCTCTCATCG 403
Db 405 TCTCTGCCCTCCTACTCTGCTGATGAGCTCTGCGACGATGCTAACCTTCGGGGTCAATG 464

QY 404 CACTGGGAGCGTACCTCTCTATGCCCCACCCAGCTTTTCCCAAGTTTTCAGTCCCA 463
Db 465 CCATCGACCGCTACTATGCTGTCTGTACCCCATGGTGATACCCCATGAAGATCACAGGA 524
QY 464 AGGGGATAGTGTGGCACTGGTGAGCACTGGGTT 498
Db 525 ACCGGGCTGTGATGGCACTTGTCTACATCTGGCTT 559

RESULT 6

US-09-030-582-1
; Sequence 1, Application US/09030582
; Patent No. 5994506
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,582
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-324
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101...1687
US-09-030-582-1

Query Match 6.6%; Score 87; DB 2; Length 2481;
Best Local Similarity 53.7%; Pred. No. 2.8e-15;
Matches 180; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 164 CCGTGGGCAATGTCTACCTACTGGCGCTTGGCCATCCAGCCCAAGCTCCGTACCCGAT 223
Db 225 CCGTGGGCAATGTCTACCTACTGGCGCTTGGCCATCCAGCCCAAGCTCCGTACCCGAT 284
QY 224 TCAACCTGCTCATAGCCAACTCAGTGGGTGATCTCTCTACTGACGCTCCCTTCAGC 283
Db 285 GCAACAAGTTCGTCTTACGCTGACTCTGTCCAACTTCTCTGCTGTGGTGTGGTGTGC 344
QY 284 CTTTCTGTGGACACCTTACCTCAGCTGCTGCGGCGACGGTGCCACCTTCTGCGAGG 343
Db 345 CTTTGTGGTGACAGCTTCCATCCGAGGGAATGGATCTTTGGTGTAGTGTGGTCAACT 404

QY 344 TATTGGGCTCCCTTTTGGCTCCAAATCTGTCTCCATCTGACCTCTGCTCATCG 403
 Db 405 TCTCTGCCCTCTCTACCTGCTGATCAGCTCTGCCAGCATGCTAACCTCGGGGTCATTG 464
 QY 404 CACTGGGAGCTACCTCTCTCAITGGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCCA 463
 Db 465 CCATCAGCGCTACTATGCTGCTCTACCCCAATGCTGTACCCCAATGAAGATCAGAGGA 524
 QY 464 AGGGGATAGTGGGCACTGGTGAGCACCTGGGTT 498
 Db 525 ACCGGGCTGTGATGGCACTGTCTACATCTGGCTT 559

RESULT 7
 PCT-US94-09051-1
 ; Sequence 1, Application PC/TUS9409051
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, ET AL.
 ; TITLE OF INVENTION: Adrenergic Receptor
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/09051
 ; FILING DATE: Submitted herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FERRARO, GREGORY D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-194
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2481 BASE PAIRS
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: SINGLE
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE: CDNA
 ; PCT-US94-09051-1

Query Match 6.6%; Score 87; DB 5; Length 2481;
 Best Local Similarity 53.7%; Pred. No. 2.8e-15;
 Matches 180; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
 QY 164 CCGTGGCAATGTGCTACCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGAT 223
 Db 225 CCGTGGCAATGTGCTACCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGAT 284
 QY 224 TCACCTGCTCATAGCCCACTACCTGCTGATCTCTCTACTGACGCTCCTTCAGC 283
 Db 285 GCACCAAGTTCGCTTCAGCGCTGACTGTGCGCACTTCCTGCTGCTGCTGCTGCTG 344
 QY 284 CTTTCTGTGGACACCTACTCCACCTGACCTGGGCGCACCGGTGCACCTCTTCGAGG 343
 Db 345 CTTTGTGGTGGACGAGCTCCATCCGAGGGAATGGATCTTTGGTGTAGTGGTGA 404
 QY 344 TATTGGGCTCCCTTTTGGCTCCAAATCTGTCTCCATCTGACCTCTGCTCATCG 403

Db 405 TCTCTGCCCTCTCTACCTGCTGATCAGCTCTGCCAGCATGCTAACCTCGGGGTCATTG 464
 QY 404 CACTGGGAGCTACCTCTCTCAITGGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCCA 463
 Db 465 CCATCAGCGCTACTATGCTGCTCTACCCCAATGCTGTACCCCAATGAAGATCAGAGGA 524
 QY 464 AGGGGATAGTGGGCACTGGTGAGCACCTGGGTT 498
 Db 525 ACCGGGCTGTGATGGCACTGTCTACATCTGGCTT 559

RESULT 8
 US-08-722-001-17
 ; Sequence 17, Application US/08722001
 ; Patent No. 5760054
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Wayne J.
 ; APPLICANT: Huff, Joel R.
 ; APPLICANT: Nerenberg, Jennie B.
 ; APPLICANT: Lee, Hee-Yoon
 ; APPLICANT: Bell, Ian M.
 ; TITLE OF INVENTION: ALPHALIC ADRENERGIC RECEPTOR ANTAGONISTS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merck & Co., Inc.
 ; STREET: 126 Lincoln Avenue
 ; CITY: Rahway
 ; STATE: New Jersey
 ; COUNTRY: United States of America
 ; ZIP: 07065
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/722,001
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/229,276
 ; FILING DATE: 14-APR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Appellina, Mary A.
 ; REGISTRATION NUMBER: 34,087
 ; REFERENCE/DOCKET NUMBER: 19169Y
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908)594-3462
 ; TELEFAX: (908)594-4720
 ; TELEX: 138825
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 921 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: both
 ; MOLECULE TYPE: CDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-722-001-17

Query Match 6.3%; Score 83; DB 1; Length 921;
 Best Local Similarity 52.1%; Pred. No. 2.5e-14;
 Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
 QY 160 GGCACCGTGGCAATGTGCTACCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACC 219
 Db 183 GCCATCGTGGCAATGTGCTACTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 242
 QY 220 CGATTCAACCTGCTCATAGCCAACTCAGCTGGTGTATCTCTCTACTGACGCTCCTT 279
 Db 243 CCCACCACTACTTCACTGTCAACCTGCGCCATGCGCGACCTGCTGTGAGCTTACCGGTC 302

280 CAGCCCTTCTGTGGACACCTACCTCCACCTGCTGGGCGACCGGTGCCACCTTCTGTC 339
303 CTGCCCCTTCTCAGCGGCCCTAGAGGTCTCGGCTACTCGGTGCTGGGGCGGATCTTCTGT 362
340 AGGTAATTGGGCTCCTCTTTTGGCTGCTCAATCTCTCTCCATCTCTGACGCTCTGCCTC 399
363 GACATCTGGGCGCGGTGGATGTCCTGTGTGACAGCGTCCATCTGAGCCTGTGGCC 422
400 ATCCCACTGGGACGCTACCTCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGT 459
423 ATCTCCATCGATCGTACATCGGGTGGCTACTCTCTGCAGTATCCACGCTGGTCAAC 482
460 GCCAAGGGGATAGTGTGGACCTGCTGGACACCTGGGTTGTGGGCGTGGCCAGCT 514
483 CGGAGGAAGGCCATCTTGGCCCTCTCAGTGTCTGGGTCTTGTCCACCGTCACT 537

RESULT 9

US-08-722-001-24
; Sequence 24, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:

APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel R.
APPLICANT: Nerenberg, Jennie B.
APPLICANT: Lee, Hee-Yoon
APPLICANT: Bell, Ian M.

TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: United States of America

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/722.001

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/229,276

FILING DATE: 14-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Appollina, Mary A.

REGISTRATION NUMBER: 34,087

REFERENCE/DOCKET NUMBER: 19169Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)594-3462

TELEFAX: (908)594-4720

TELEX: 138825

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 1567 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-722-001-24

Query March

Best Local Similarity 52.1%; Score 83; DB 1; Length 1567;

Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY

160 GGCACCGTGGCAATGTGCTCACCTACTGCGCTTGGCGCATCCAGCCCAAGCTCCGTACC 219

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280 CAGCCCTTCTCTGTGGACACCTACCTCCACTGACCTGGCGCACCGGTGCCACCTTCTGC 339
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340 AGGGTATTGTGGCTCCTCTCTTTTGGCTTCCCAATTTCTGTCTCCATCTGACCTCTGGCTC 399
363 GACATCTGGGCGCGGTGGATGTCCTGTGTGTCACAGGCTCCATCTGAGCCTGTGGCC 422
400 ATCGCAGCTGGGACGCTACTCTCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGT 459
423 ATCTCCATCGATCGCTACATCGGGTGGCTACTCTCTGCAGTATCCACGCTGGTCAAC 482
460 GCCAAGGGGATAGTGTGGCACTGGTGGACACCTGGGTTGTGGGCGTGGCCAGCT 514
483 CGGAGGAAGGCCATCTTGGCCCTCTCAGTGTCTGGGTCTTGTCCACCGTCACT 537

RESULT 10

US-08-334-698-3

; Sequence 3, Application US/08334698

; Patent No. 5556753
; GENERAL INFORMATION:

APPLICANT: Jonathan A. Bard et al.

TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic

RECEPTORS AND USES THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/334,698

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/952,798

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 376901

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: (212) 422523 COOP UI

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1738 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: N

ANTI-SENSE: N

FEATURE:

NAME/KEY: CDS

LOCATION: 124..1683

OTHER INFORMATION:

US-08-334-698-3

Query Match 6.3%; Score 83; DB 1; Length 1738;
Best Local Similarity 52.1%; Pred. No. 3.5e-14;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
QY 160 GGACCGTGGGCAATGTCTACACCTGCTGGCTGGCCATCCAGCCCAAGCTCCGTACC 219
Db 298 GCATCTGTGGGCAATCTAGTCACTCTGTCTGGCTGCAACCGGCACCTGGGACG 357
QY 220 CGATTCAACCTGCTATAGCAACCTCACTGGCTGATCTCTTACTGACGCTCTCTT 279
Db 358 CCACCAACTACTTCTATGCAACCTGGCCATGGCCGACCTGTTGAGCTTCAACGTC 417
QY 280 CAGCCTCTCTGTGGACACCTTCACTGCACTGGCGGACCGGTCACCTTCTGC 339
Db 418 CTGCTCTCTCAGCGGCTCTAGAGTCTGCGCTACTGGTCTGGGCGGATCTTCTGT 477
QY 340 AGGTATTTGGGCTCTCTCTTTTGGCTCCAAATCTGTCTCCATCTGACCTCTGCTC 399
Db 478 GACATCTGGGACCGCTGATGCTCTGTGCAAGCGTCCATCTGAGCCTGTGCGGC 537
QY 400 ATGCACTGGGACGCTACCTCTCATGCGCCACCTTAAGCTTTTCCCAAGTTTTCAGT 459
Db 538 ATCTCATCGATCGCTACATCGGGTGGCTACTCTCTGAGTATCCCAAGCTTGTAC 597
QY 460 GCCAAGGGATAGTGTGCTGCACTGTGACACCTGCTGGGTTTGTGGGCTGGCCAGCT 514
Db 598 CGAGGAGGCGCATCTTGGCGCTGCTCAGTGTGCGTCTGTGCGACCGTCACT 652

RESULT 11
US-08-228-932-3
Sequence 3, Application US/08228932
Patent No. 5578611
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
APPLICANT: Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
TITLE OF INVENTION: PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,932
FILING DATE: 13-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N

ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-228-932-3

Query Match 6.3%; Score 83; DB 1; Length 1738;
Best Local Similarity 52.1%; Pred. No. 3.5e-14;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
QY 160 GGACCGTGGGCAATGTCTACACCTGCTGGCTGGCCATCCAGCCCAAGCTCCGTACC 219
Db 298 GCATCTGTGGGCAATCTAGTCACTCTGTCTGGCTGCAACCGGCACCTGGGACG 357
QY 220 CGATTCAACCTGCTATAGCAACCTCACTGGCTGATCTCTTACTGACGCTCTCTT 279
Db 358 CCACCAACTACTTCTATGCAACCTGGCCATGGCCGACCTGTTGAGCTTCAACGTC 417
QY 280 CAGCCTCTCTGTGGACACCTTCACTGCACTGGCGGACCGGTCACCTTCTGC 339
Db 418 CTGCTCTCTCAGCGGCTCTAGAGTCTGCGCTACTGGTCTGGGCGGATCTTCTGT 477
QY 340 AGGTATTTGGGCTCTCTCTTTTGGCTCCAAATCTGTCTCCATCTGACCTCTGCTC 399
Db 478 GACATCTGGGACCGCTGATGCTCTGTGCAAGCGTCCATCTGAGCCTGTGCGGC 537
QY 400 ATGCACTGGGACGCTACCTCTCATGCGCCACCTTAAGCTTTTCCCAAGTTTTCAGT 459
Db 538 ATCTCATCGATCGCTACATCGGGTGGCTACTCTCTGAGTATCCCAAGCTTGTAC 597
QY 460 GCCAAGGGATAGTGTGCTGCACTGTGACACCTGCTGGGTTTGTGGGCTGGCCAGCT 514
Db 598 CGAGGAGGCGCATCTTGGCGCTGCTCAGTGTGCGTCTGTGCGACCGTCACT 552

RESULT 12
US-08-468-939-3
Sequence 3, Application US/08468939
Patent No. 5714381
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1683
; OTHER INFORMATION:
US-08-468-939-3

Query Match      6.3%; Score 83; DB 1; Length 1738;
Best Local Similarity 52.1%; Pred. No. 3.5e-14;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 160 GGCACCGTGGGCAATGTGCTCACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACC 219
Db 298 GCCATCGTGGGCAACATCTAGTCACTTGTCTGTGGCTGCAACCGGCACCTGGCGACG 357
QY 220 CGATTCAACCTGCTCATAGCCAACTCCTAGTCACTTGTCTGTGGCTGCAACCGGCACCTGGCGACG 357
Db 358 CCCACCAACTACTTCAATTTGCAACCTGGCCATGGCCGACCTGCTGTGAGCTTCCCGTC 417
QY 280 CAGCCCTTCTCTGTGGACACCTACTCCCTCCTGCACTGGCCGACCGGTGCCACCTTCTGC 339
Db 418 CTGCCCCTCTCAGCGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGCGGATCTTCTGT 477
QY 340 AGGGTATTGGGCTCCTCTTTTGGCTCCCAATTCGTCTCCATCTGACCTGACCTCTGCCTC 399
Db 478 GACATCTGGGACCGGTGGATGCTGCTGTGTCGACAGGTCATCTGAGCCCTGTGGGCC 537
QY 400 ATCCACTGGGACCTACCTCCTCATTCATCCACCCCTAAGCTTTTCCCAAGTTTTCAGT 459
Db 538 ATCTCCATCGATCGTACATCGGGGTGCGCTACTCTCTGCAGTATCCACCGTGGTCACC 597
QY 460 GCCAAGGGGATAGTCTGGCACTGGTGACACCTGGGTGTGGCGGTGGGCCAGCT 514
Db 598 CGGAGGAAGGCCATCTTGGCGCTGCTCAGTGTCTGGGTCTGTGCCACCGTCATCT 652

RESULT 13
US-08-406-855A-3
; Sequence 3, Application US/08406855A
; Patent No. 5861309
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,855A
; FILING DATE: 21-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1683
; OTHER INFORMATION:
US-08-406-855A-3

Query Match      6.3%; Score 83; DB 2; Length 1738;
Best Local Similarity 52.1%; Pred. No. 3.5e-14;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 160 GGCACCGTGGGCAATGTGCTCACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACC 219
Db 298 GCCATCGTGGGCAACATCTAGTCACTTGTCTGTGGCTGCAACCGGCACCTGGCGACG 357
QY 220 CGATTCAACCTGCTCATAGCCAACTCCTAGTCACTTGTCTGTGGCTGCAACCGGCACCTGGCGACG 357
Db 358 CCCACCAACTACTTCAATTTGCAACCTGGCCATGGCCGACCTGCTGTGAGCTTCCCGTC 417
QY 280 CAGCCCTTCTCTGTGGACACCTACTCCCTCCTGCACTGGCCGACCGGTGCCACCTTCTGC 339
Db 418 CTGCCCCTCTCAGCGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGCGGATCTTCTGT 477
QY 340 AGGGTATTGGGCTCCTCTTTTGGCTCCCAATTCGTCTCCATCTGACCTGACCTCTGCCTC 399
Db 478 GACATCTGGGACCGGTGGATGCTGCTGTGTCGACAGGTCATCTGAGCCCTGTGGGCC 537
QY 400 ATCCACTGGGACCTACCTCCTCATTCATCCACCCCTAAGCTTTTCCCAAGTTTTCAGT 459
Db 538 ATCTCCATCGATCGTACATCGGGGTGCGCTACTCTCTGCAGTATCCACCGTGGTCACC 597
QY 460 GCCAAGGGGATAGTCTGGCACTGGTGACACCTGGGTGTGGCGGTGGGCCAGCT 514
Db 598 CGGAGGAAGGCCATCTTGGCGCTGCTCAGTGTCTGGGTCTGTGCCACCGTCATCT 652

RESULT 14
US-08-722-190-3
; Sequence 3, Application US/08722190
; Patent No. 5990128
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Fortay, George
; APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,190
; FILING DATE: 4-APR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
; TELECOMMUNICATION INFORMATION:
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Job time : 105.224 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:04:24 ; Search time 5339.89 Seconds
(without alignments)
10641.181 Million cell updates/sec

Title: US-10-029-436-1

Perfect score: 1311

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Scoring table: IDENTITY_NUC

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Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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40: em_htgo_mus:*

41: em_htgo_other:*

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and is derived by analysis of the total score distribution.

SUMMARIES

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5	1256.4	95.8	1546	6	AX549299	Sequence
6	1256.4	95.8	1546	9	AF282693	Homo sapi
7	1256.4	95.8	1595	6	AX247564	Sequence
8	1191	90.8	1191	6	BD144298	Novel G-p
9	1191	90.8	1191	9	AB083586	Homo sapi
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11	897	68.4	1574	10	BC023249	Mus muscu
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23	87.8	6.7	2400	9	AX122656	Homo sapi
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37	83	6.3	1738	6	AR228241	Sequence
38	83	6.3	1738	6	AR270839	Sequence
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ALIGNMENTS

RESULT 1

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC078778 Homo sapiens 141003 bp DNA linear PRI 21-FEB-2003
Human BAC Library) complete sequence.

AC078778 GI:23307958

HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 141003)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsebrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,

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Qy	601	ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC	660
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Qy	661	ATCCACCGCCAGGTCAAACGAGCAGCACAGGCATCTGGACCAATACAAGTTCCGACAGGCA	720
Db	6576	ATCCACCGCCAGGTCAAACGAGCAGCACAGGCATCTGGACCAATACAAGTTCCGACAGGCA	6635
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               Homo sapiens
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               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               1 (bases 1 to 1493)
               Wittenberger,T., Schaller,H.C. and Hellebrand,S.
               An expressed sequence tag (EST) data mining strategy succeeding in
               the discovery of new G-protein coupled receptors
               J. Mol. Biol. 307 (3), 799-813 (2001)
               21172992
               11273702
               2 (bases 1 to 1493)
               Wittenberger,T. and Hellebrand,S.
               Direct Submission
               Submitted (28-MAR-2000) ZMNH, Institut fuer
               Entwicklungsneurobiologie, Martinistr. 52, Hamburg 20246, Germany
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                  /gene="GPR84"
                  69. .1259
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1498)
AUTHORS Sathie G.Madhusudan., Fuetterer, W.S., Bergsma, D. John. and Ellis, C.
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receptor
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SOURCE	Hom sapiens (human)
ORGANISM	Hom sapiens
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AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udwin, T.B., Toshiyuki, S., Mancini, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Buetow, K.H., Krzywinski, M.I., Skalska, J., Smolnik, D.E., Schnerbach, A., Schein, J.E., Jones, S.J., and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 1535)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-sbc.stanford.edu Contact: (Dickson, Mark) mc3@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov Series: IPAL Plate: 35 Row: k Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9966838. Location/Qualifiers 1..1535 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:22224 IMAGE:4279185" /tissue_type="Brain, primitive neuroectodermal" /clone_lib="NIH_MGC_56" /lab_host="DH10B" /note="Vector: pDNR-LIB" 1..1535 /gene="GPR84" /note="synonyms: EX33, GPCR4" /db_xref="LOCUSID:53831" /db_xref="MIM:606383" 101..1291 /codon_start=1 /product="inflammation-related G protein-coupled receptor EX33" /protein_id="AAH20614.1"
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LOCUS Homo sapiens inflammation-related G protein-coupled receptor EX33
DEFINITION (EX33) mRNA, complete cds.
ACCESSION AF282693
VERSION AF282693.1 GI:9652260
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1546)
Yousefi, S., Cooper, P.R., Potter, S.L., Mueck, B. and Jarai, G.
Cloning and expression analysis of a novel G-protein-coupled
receptor selectively expressed on granulocytes
J. Leukoc. Biol. 69 (6), 1045-1052 (2001)
MEDLINE 21297471
PubMed 11404393
REFERENCE 2 (bases 1 to 1546)
Yousefi, S., Cooper, P.R., Mueck, B., Potter, S. and Jarai, G.
Direct Submission
Submitted (26-JUN-2000) NHRC, Wimblerhurst, Horsham, West Sussex
RH12 5AB, UK
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 95.8%; Score 1256.4; DB 9; Length 1546;
Best Local Similarity 99.9%; Pred. No. 4.2e-313;
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 DEFINITION Sequence 1 from Patent WO0166597.
 ACCESSION AX247564

VERSION AX247564.1 GI:15862254
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Jarai, G., Cooper, P.R. and Yousefi, S.
 TITLE Inflammation-related gene
 JOURNAL Patent: WO 0166597-A 13-SEP-2001;
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LOCUS BD144298 1191 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel G-protein coupled receptors.
ACCESSION BD144298
VERSION BD144298.1 GI:27850056
KEYWORDS JP 2002112793-A/23.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1191)
AUTHORS Haga,T., Takeda,S. and Miyake,N.
TITLE Novel G-protein coupled receptors
JOURNAL Patent: JP 2002112793-A 23 16-APR-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002112793-A/23
PD 16-APR-2002
PF 09-FEB-2001 JP 2001034434
PI TATSUYA HAGA,SHIGEKI TAKEDA,NARIKI MIYAKE
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 DEFINITION Homo sapiens GPCR gene for putative G-protein coupled receptor,
 complete CDS, clone:hgPCR4.
 ACCESSION AB083586
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 1 Takeda, S., Kadowaki, S., Haga, T., Takaesu, H. and Mitaku, S.
 Identification of G protein-coupled receptor genes from the human
 genome sequence
 JOURNAL Unpublished
 2 (bases 1 to 1191)
 Takeda, S., Kadowaki, S., Haga, T., Takaesu, H. and Mitaku, S.
 Direct Submission
 JOURNAL Submitted (10-APR-2002) Shigeaki Takeda, Gunma University,
 Department of Biological and Chemical Engineering, Faculty of
 Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan
 (E-mail:stakeda@ce.gunma-u.ac.jp, Tel:+81-277-30-1434,
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 Best Local Similarity 100.0%; Pred. No. 2.5e-296;
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Qy 61 ATGTGGACAGCTCTGACGGCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 120
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  High Throughput Mouse Sequencing
  Unpublished
  2 (bases 1 to 207421)
  Grills, G., Han, J., Montgomery, K.T., Lee, B., Long, J., Pomerantz, R.,
  Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M.
  and Kucherlapati, R.
  Direct Submission
  Submitted (19-JAN-2000) Department of Molecular Genetics, Albert
  Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
  Bronx, NY 10461, USA
  On Aug 9, 2001 this sequence version replaced gi:14717145.
  -----Genome Center
  Center: Harvard Partners Genome Center
  Center Code: HPGC
  Web site: http://www.hpcgg.org/Sequence/mouse.html
  Contact: hpgc@mcgdel.mgh.harvard.edu
  -----Summary Statistics
  Center project name: AAR
  Sequencing vector: pUC18; L08752
  Chemistry: Dye-terminator Big Dye, 100%
  *Consensus quality: 193187 at least Q20
  *Consensus quality: 190826 at least Q30
  *Consensus quality: 186718 at least Q40
  Estimated insert size: agarose-PF - N/A
  **Estimated insert size: 206981 - sum-of-contigs
  Quality coverage: agarose-PF - N/A
  Quality coverage: 6.5 x in Q20 bases; sum-of-contigs estimation
  -----
  * NOTE: This is a 'working draft' sequence. It currently
  * consists of 23 contigs. The true order of the pieces
  * is not known and their order in this sequence record is
  * arbitrary. Gaps between the contigs are represented as
  * runs of N, but the exact sizes of the gaps are unknown.
  * This record will be updated with the finished sequence
  * as soon as it is available and the accession number will
  * be preserved
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  * 1 38304: contig of 38304 bp in length
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  * 89010 89029: gap of unknown length
  * 89030 108492: contig of 19463 bp in length
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  * 108513 120232: contig of 11720 bp in length
  * 120233 120252: gap of unknown length
  * 120253 131080: contig of 10828 bp in length
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  * 142710 155481: contig of 12772 bp in length
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  * 164035 171335: contig of 7301 bp in length
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  * 202596 203643: contig of 1048 bp in length
  * 203644 203663: gap of unknown length
  * 203664 204541: contig of 878 bp in length
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  * 204562 204816: contig of 255 bp in length
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  * 204837 204909: contig of 73 bp in length
  * 204910 204929: gap of unknown length
  * 204930 206958: contig of 2029 bp in length
  * 206959 206978: gap of unknown length
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[illegible][illegible]

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 DEFINITION complete cds.
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 VERSION AF272948.1 GI:12711474
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 Wittenberger, T., Schaller, H.C. and Hellebrand, S.
 An expressed sequence tag (EST) data mining strategy succeeding in
 the discovery of new G-protein coupled receptors
 J. Mol. Biol. 307 (3), 799-813 (2001)
 MEDLINE 21172992
 PUBMED 11273702
 REFERENCE 2 (bases 1 to 1611)
 Wittenberger, T. and Hellebrand, S.
 Direct Submission
 Submitted (29-MAY-2000) ZMNH, Institut fuer
 Entwicklungsneurobiologie, Martinistr. 52, Hamburg 20246, Germany
 JOURNAL Location/Qualifiers
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 ORIGIN
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 124 CTTCACTCTCATCATGTGGAACAGCTCTGAGTCCAACTTCTCTCTACCATGAGCTCTG 183
 107 TGTGGGCTATCGATTATGTTGCAAGTGTGAGTGGGGGTGGTGGTGTGACAGGACCG 166
 184 TGTGGGCTATCGATTATGTTGCAAGTGTGAGTGGGGGTGGTGGTGTGACAGGACCG 243
 167 TGGGCAATGCTCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 226
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 227 ACCTGTCTATGCAACCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 286
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QY 347 TTGGCT 406
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 QY 407 TGGGACGCTACT 466
 DB 484 TAGGACGCTACT 543
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 DB 604 GGAATGTTTTTGTCTTGTGTGCACTTGTGTGCACTTGTGTGCACTTGTGTGCACTTGTGT 663
 QY 587 GGCCTTACACCACT 646
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 DB 1324 ATTAAGCTAT 1334
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 DEFINITION AC126846
 ACCESSION AC126846
 VERSION AC126846.2 GI:22772739
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.


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sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
-----
Center project name: GDR
Center clone name: CH230-11M7
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 22716 bases at least Q40
Consensus quality: 225022 bases at least Q30
Consensus quality: 226487 bases at least Q20
Estimated insert size: 247241; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* * NOTE: this is a 'working draft' sequence. It currently
* * consists of 1 contigs. Gaps between the contigs
* * are represented as runs of N. The order of the pieces
* * is believed to be correct as given, however the sizes
* * of the gaps between them are based on estimates that have
* * provided by the submitter.
* * This sequence will be replaced
* * by the finished sequence as soon as it is available and
* * the accession number will be preserved.
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337; Conservative 0; Mismatches 225; Indels 1; Gaps 1;
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Qy 430 CACCTTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGAGTGTGCTGGCACTGCTGACG 489

Db 55045 CACCTTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGAGTGTGCTGGCACTGCTGACG 55104

Qy 490 ACCTGGGTGTGGGGTGGCGGCTTGTCTCCCTCTGCTGCTATTTATATCTCTGTTACCT 549

Db 55105 AGCTGGGTGTGGGGTGGCGGCTTGTCTCCCTCTGCTGCTATTTATATCTCTGTTACCT 55164

Qy 550 GTAGTCTCACCTGACGCTTTGACCGCATCCGAGCGCGGCTTACACCATCCTCATG 609

Db 55165 GTTGTCTCACCTGACGCTTTGACCGCATCCGAGCGCGGCTTACACCATCCTCATG 55224

Qy 610 GGCATCTACTTTGTCTTGGCTCAGCAGTGTGGCATCTTCTTATTCCTCATCCACCGC 669

Db 55225 GGCATCTACTTTGTCTTGGCTCAGCAGTGTGGCATCTTCTTATTCCTCATCCACCGC 55284

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RESULT 14
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DEFINITION Homo sapiens clone RP11-1009, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC016463

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

AC016463.3 GI:7144792

HTG; HTGS_PHASE0.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 141003)

Birken, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-1009

Unpublished

2 (bases 1 to 141003)

Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hegos, B., Heaford, A., Horton, L., LeHoczy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (30-NOV-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 3, 2000 this sequence version replaced gi:6910791.

All repeats were identified using RepeatMasker.

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: U3130

Center clone name: 10_0_9

* NOTE: This record contains 152 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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* 966 1849: contig of 884 bp in length

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* 3961 4824: contig of 864 bp in length

* 4825 4924: gap of 100 bp

* 4925 5792: contig of 868 bp in length

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* 8753 9726: contig of 874 bp in length

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QY 577 ATCCGAGGCGGCGCTTACACCATCTCATGGCATCTACTTGTGCTTGGGCTCAGC 636
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DEFINITION Endogeneous, constitutionally activated protein G-coupled orphan
receptor.
ACCESSION BD229108
VERSION BD229108.1 GI:33038878
KEYWORDS JP 2002521681-A/20.
SOURCE synthetic construct
ORGANISM Behan,D.P., Chalmers,D.T., Liaw,C., Lin,I.L., Lowitz,K. and Chen,R.
REFERENCE 1 (bases 1 to 1382)
AUTHORS Behan,D.P., Chalmers,D.T., Liaw,C., Lin,I.L., Lowitz,K. and Chen,R.
TITLE Endogeneous, constitutionally activated protein G-coupled orphan
receptor
JOURNAL Patent: JP 2002521681-A 20 16-JUL-2002;
ARENA PHARMACEUTICALS INC
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PN JP 2002521681-A/20
PD 16-JUL-2002
PF 30-JUL-1999 JP 2000562393
PR 31-JUL-1998 US 60/094879,30-OCT-1998 US 60/106300 PR
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DOMINIC P BEHAN,DEREK T CHALMERS,CHEN LIAW,I LIN LIN,KEVIN PI
LOWITZ,
PI RUOPING CHEN
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CC Description of Artificial Sequence: Synthetic Sequence FH
Key Location/Qualifiers
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FT /organism='Artificial Sequence'.
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Best Local Similarity 53.7%; Pred. No. 1.7e-11;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	1306	99.6	2046	5 AAS29737	Aas29737 Human end
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28	355	27.1	483	4 AAS28939	Aas28939 cDNA enco
29	355	27.1	483	4 AAS30167	Aas30167 cDNA enco
30	355	27.1	483	4 AAS34782	Aas34782 cDNA enco
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34	355	27.1	483	5 AAS29521	Aas29521 Human end
35	355	27.1	483	6 ABT07774	Abt07774 Novel hum
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ALIGNMENTS

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DT 03-OCT-2003 (first entry)
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DE Human hpl5a receptor coding sequence.
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KW Human; hpl5a; receptor; G-protein coupled receptor; cardiant;
KW gastrointestinal; gene therapy; gene; ds.
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OS Homo sapiens.
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FH Key Location/Qualifiers
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XX
PN WO2003054540-A1.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040612.
XX
PR 19-DEC-2001; 2001US-00029436.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Smith KE, Weinshank R;
XX
DR WPI: 2003-559173/52.
XX
DR P-PSDB; ABR52422.
XX
PT New recombinant nucleic acid, useful for preparing a composition for
PT treating disorders linked to human hpl5a receptor e.g. cardiovascular or
PT gastrointestinal disorders.
XX
PS Claim 1; Fig 1A-B; 98pp; English.
XX
CC The present sequence is that of nucleic acid encoding a human orphan G-
CC protein coupled receptor, designated hpl5a. The sequence was initially
CC identified in a human placenta genomic library using probes representing
CC transmembrane domains III, V and VI of human serotonin 5-HT2beta
CC receptor. The endogenous ligand for hpl5a is likely to be a

CC neuromodulator since the receptor is present in several regions of the
 CC human brain. The invention provides hpl5a nucleic acids, vectors, host
 CC cells, antibodies, probes, antisense oligonucleotides, transgenic non-
 CC human animals, methods of isolating the receptor, methods of treating an
 CC abnormality that is associated with activity of hpl5a e.g. cardiovascular
 CC or gastrointestinal disorders, and methods of determining binding of
 CC compounds to hpl5a
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Sequence 1311 BP; 266 A; 409 C; 315 G; 321 T; 0 U; 0 Other;

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 XX 21-NOV-2001 (first entry)
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 DE Human; uterine motility-association disorder; uterus; pregnancy; labour;
 KW menstrual cycle; gene therapy; ds.
 XX Homo sapiens.

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 XX WO200155201-A1.
 PN
 XX 02-AUG-2001.
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 XX 17-JAN-2001; 2001WO-US0001317.
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 PR 05-JAN-2001; 2000US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI; 2001-488777/53.
 XX
 PT New nucleic acid molecules encoding 49 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives.
 XX
 PS Disclosure; SEQ ID NO 130; 524pp; English.
 XX
 CC The present invention relates to the isolation of novel human uterine
 CC motility-association polypeptides (AAU8094-AAU8152), and cDNA and
 CC genomic sequences encoding for these polypeptides. The sequences of the
 CC invention are useful in the diagnosis, treatment, prevention and/or
 CC prognosis of diseases associated with uterine motility such as pregnancy
 CC and labour, and menstrual disorders. The polynucleotide sequences of the
 CC invention are also useful in gene therapy. AA828995-AA829020 represent
 CC genomic sequences encoding for novel human uterine motility-association
 CC polypeptides. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences
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Query Match 99.6%; Score 1306; DB 4; Length 2046;
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PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-488787/53.
XX
XX New polynucleotides and polypeptides, useful for diagnosing, treating,
PT preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte
PT imbalance or neoplastic disorders, autoimmune diseases, cancers.
XX
XX Claim 1; SEQ ID NO 155; 506pp; English.
XX
XX The invention relates to novel nucleic acids and polypeptides useful for
CC diagnosing, treating, preventing and/or prognosing disorders related to
CC these polypeptides. The polynucleotides are especially useful in the
CC diagnosis, prognosis, prevention and/or treatment of diseases which
CC include kidney disorders (e.g. renal failure or nephritis),
CC cardiovascular disorders (e.g. hypertension or myocardial infarction),
CC blood disorders (e.g. anaemia or blood coagulation disorders),
CC electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia),
CC neoplastic disorders (e.g. nephroma or renal cell cancer), autoimmune
CC diseases, cancers, inflammatory diseases, reproductive system disorders,
CC endocrine disorders, neural activity and neurological disorders, wound
CC healing and respiratory disorders. AAS30165-AAS30251 represent the novel
CC human renal and cardiovascular-associated nucleic acid sequences of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at: ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;
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Query Match 99.6%; Score 1306; DB 4; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 AC AAS35064;
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 DT 04-DEC-2001 (first entry)
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 DE DNA #14 encoding human neoplastic disease associated polypeptide.
 XX
 DE Human; neoplastic disease associated polypeptide; cancer; gene therapy;
 KW hyperproliferative disorder; neural disorder; immune system disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200155163-A1.
 XX
 PD 02-AUG-2001.
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 PF 17-JAN-2001; 2001WO-US001358.
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DT 07-NOV-2001 (first entry)
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KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
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PD 09-AUG-2001.
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PF 17-JAN-2001; 2001WO-US001354.
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PR 14-SEP-2000; 2000US-0233065P.
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PR 21-SEP-2000; 2000US-0234274P.
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PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
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PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
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PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
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PR 01-NOV-2000; 2000US-024617P.
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PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
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PR 17-NOV-2000; 2000US-0249213P.
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PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.

PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
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PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251475P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 32393; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention
XX
XX
XX Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;

Query Match 99.6%; Score 1306; DB 4; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATGCTAGGTTCTGATTCCTCTTCTTCCACCTCTGCTCTTTAGCCTCTATC 60
DB 577 TTGAATGCTAGGTTCTGATTCCTCTTCCACCTCTGCTCTTTAGCCTCTATC 636
QY 61 ATGTGGAACAGCTCTGACGCAACTTCTCTGTGACCATGATGTGTGGTGGTATCGT 120
DB 637 ATGTGGAACAGCTCTGACGCAACTTCTCTGTGACCATGATGTGTGGTGGTATCGT 696
QY 121 TATGTTGCAGTACTGCTGGGGGTGTGTGCTGTGACGACCACTGGGGAATGTGCTC 180
DB 697 TATGTTGCAGTACTGCTGGGGGTGTGTGCTGTGACGACCACTGGGGAATGTGCTC 756
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGTCCGATCCCGATTCAACTGCTCATAGCC 240
DB 757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGTCCGATCCCGATTCAACTGCTCATAGCC 816
QY 241 AACCTACACTGGCTGATCTCTCTACTGACGCTCTCTTACGCGCTTCTCTGTGACACC 300
DB 817 AACCTACACTGGCTGATCTCTCTACTGACGCTCTCTTACGCGCTTCTCTGTGACACC 876

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301	QY	TACCTCACCCTGACTGCTGGCGACCGGTGGCCACCTTCTGACGGGTATTTTGGGCTCCTCCTT	360
877	Db	TACCTCACCCTGCACTGGCGCACCGGTGGCCACCTTCTGACGGGTATTTTGGGCTCCTCCTT	936
361	QY	TTTGGCTCCAAATCTGTCTCATCTCTGACCTCTGCTCATCGCACTGGGACGCTACCTC	420
937	Db	TTTGGCTCCAAATCTGTCTCATCTCTGACCTCTGCTCATCGCACTGGGACGCTACCTC	996
421	QY	CTCATTTGCCACCACTTAAGCTTTTTCCTCCCAAGTTTTCAGTGCACGAAGGGGATAGTGTCTGGCA	480
997	Db	CTCATTTGCCACCACTTAAGCTTTTTCCTCCCAAGTTTTCAGTGCACGAAGGGGATAGTGTCTGGCA	1056
481	QY	CTGGTGAGCACTTGGGTGTGGGCGTGGCCAGACTTTGCTCCCTCTGGCCCTATTATATATC	540
1057	Db	CTGGTGAGCACTTGGGTGTGGGCGTGGCCAGACTTTGCTCCCTCTGGCCCTATTATATC	1116
541	QY	CTGGTACTGTAGTCTGCACTCTGAGACTTTTTCAGCAATCCGAGCGCGGCTTACACGACC	600
1117	Db	CTGGTACTGTAGTCTGCACTCTGAGACTTTTTCAGCAATCCGAGCGCGGCTTACACGACC	1176
601	QY	ATCCTCATGGGCATCTACTTTGTCTTGGCTCAGCAGTGTGGCACTTCTATTTGGCTC	660
1177	Db	ATCCTCATGGGCATCTACTTTGTCTTGGCTCAGCAGTGTGGCACTTCTATTTGGCTC	1236
661	QY	ATCCACGCCAGGTTCAACGAGCAGCACAGGCACTGGACCAATACAAAGTTGGCAGCAGGCA	720
1237	Db	ATCCACGCCAGGTTCAACGAGCAGCACAGGCACTGGACCAATACAAAGTTGGCAGCAGGCA	1296
721	QY	AGCATCCACTCCAAACCATGTGGCCAGGACATGATAGGCCCATGCTGTGTCTTTCCAGGAG	780
1297	Db	AGCATCCACTCCAAACCATGTGGCCAGGACATGATAGGCCCATGCTGTGTCTTTCCAGGAG	1356
781	QY	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGTAGGGGATTTTCATCTGAGCCAGTCACT	840
1357	Db	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGTAGGGGATTTTCATCTGAGCCAGTCACT	1416
841	QY	GCTTCCACCACCCAGACCTCTGGAAGGGGACTCATCAGAAGTGGGAGACCAAGATCAACAGC	900
1417	Db	GCTTCCACCACCCAGACCTCTGGAAGGGGACTCATCAGAAGTGGGAGACCAAGATCAACAGC	1476
901	QY	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCCAAGCCA	960
1477	Db	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCCAAGCCA	1536
961	QY	ATTAAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCCGAATG	1020
1537	Db	ATTAAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCCGAATG	1596
1021	QY	TGTTTTGTGTGTCTCTCTTTTGGCTCGAGTACATCCCTCTTGTGTCTCAACATT	1080
1597	Db	TGTTTTGTGTGTCTCTCTTTTGGCTCGAGTACATCCCTCTTGTGTCTCAACATT	1656
1081	QY	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTCTGTCGCAACCTCACTGTG	1140
1657	Db	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTCTGTCGCAACCTCACTGTG	1716
1141	QY	CTCAATGGTTGCATCAACCCCTGTGCTCTATGACGCCATGAACCGCCAAATTCGCCCAAGCA	1200
1717	Db	CTCAATGGTTGCATCAACCCCTGTGCTCTATGACGCCATGAACCGCCAAATTCGCCCAAGCA	1776
1201	QY	TATGGGCTCCATTTTAAAGAGAGGCGCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1260
1777	Db	TATGGGCTCCATTTTAAAGAGAGGCGCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1836
1261	QY	CCTAGTCCACAGAAATTCAGGACTGTCTCTCTCCAGGACCAAGTGGC	1306
1837	Db	CCTAGTCCACAGAAATTCAGGACTGTCTCTCTCCAGGACCAAGTGGC	1882

ABR06789;
10-JAN-2002 (first entry)
Human genomic DNA SEQ ID NO: 875.
Human; gene therapy; neural disorder; immune system disorder;
muscular disorder; reproductive disorder; gastrointestinal disorder;
pulmonary disorder; cardiovascular disorder; renal disorder;
proliferative disorder; inflammation; ds.
Homo sapiens.

QY	601	ATCCTCATGGGCATCTACTTTGCTTGGGCTAGCAGTGTGGCATCTTCTATTGCTC	660	PN	XX	WO200155318-A2.
Db	1177	ATCCTCATGGGCATCTACTTTGCTTGGGCTAGCAGTGTGGCATCTTCTATTGCTC	1236	XX	XX	02-AUG-2001.
QY	661	ATCCACCGCCAGGTCAACAGCAGCAGCAGCAGTGGACCAATACAGTTGCGACAGGCA	720	PF	XX	17-JAN-2001; 2001WO-US001332.
Db	1237	ATCCACCGCCAGGTCAACAGCAGCAGCAGCAGTGGACCAATACAGTTGCGACAGGCA	1296	PR	PR	31-JAN-2000; 2000US-0179065P.
QY	721	AGCATCACTCCACATGTGGCCAGCAGCAGTATGAGCCCATGCTGCTGTTTCCAGGAG	780	PR	PR	04-FEB-2000; 2000US-0180638P.
Db	1297	AGCATCACTCCACATGTGGCCAGCAGCAGTATGAGCCCATGCTGCTGTTTCCAGGAG	1356	PR	PR	22-FEB-2000; 2000US-0184664P.
QY	781	CTGACAGCAGGTTAGCATCAGAGGAGCCAGTATGAGGGGATTTTCATCTGAGCCAGTCAGT	840	PR	PR	04-MAR-2000; 2000US-0186350P.
Db	1357	CTGACAGCAGGTTAGCATCAGAGGAGCCAGTATGAGGGGATTTTCATCTGAGCCAGTCAGT	1416	PR	PR	16-MAR-2000; 2000US-0189874P.
QY	841	GCTGCCACCCAGCAGCAGTGGAGGGGACTCATCAGAGTGGAGACCAAGTCAACAGC	900	PR	PR	17-MAR-2000; 2000US-0190076P.
Db	1417	GCTGCCACCCAGCAGCAGTGGAGGGGACTCATCAGAGTGGAGACCAAGTCAACAGC	1476	PR	PR	18-APR-2000; 2000US-0198123P.
QY	901	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGCCCAAGCCA	960	PR	PR	19-MAY-2000; 2000US-0205515P.
Db	1477	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGCCCAAGCCA	1536	PR	PR	07-JUN-2000; 2000US-0209467P.
QY	961	ATTAAAGAGCAGAGAGTCCGGATTTTCATTCGGAATTTGGGAAGGTGACTCGAATG	1020	PR	PR	28-JUN-2000; 2000US-0214886P.
Db	1537	ATTAAAGAGCAGAGAGTCCGGATTTTCATTCGGAATTTGGGAAGGTGACTCGAATG	1596	PR	PR	30-JUN-2000; 2000US-0215135P.
QY	1021	TGTTTTCTGTTCCTCTGCTTGGCCCTGAGCTACATCCCTTCTGCTGCTCAACAT	1080	PR	PR	07-JUL-2000; 2000US-0216647P.
Db	1597	TGTTTTCTGTTCCTCTGCTTGGCCCTGAGCTACATCCCTTCTGCTGCTCAACAT	1656	PR	PR	07-JUL-2000; 2000US-0216880P.
QY	1081	CTGATGCCAGAGTCCAGGCTCCCGGGTGTCCACATGTTCTGCCAACCTCACTG	1140	PR	PR	11-JUL-2000; 2000US-0217487P.
Db	1657	CTGATGCCAGAGTCCAGGCTCCCGGGTGTCCACATGTTCTGCCAACCTCACTG	1716	PR	PR	11-JUL-2000; 2000US-0217496P.
QY	1141	CTCAATGGTTCATCACTCCCTGTCTATGAGCCATGACCCCAATTCGCCCAAGCA	1200	PR	PR	14-JUL-2000; 2000US-0218290P.
Db	1717	CTCAATGGTTCATCACTCCCTGTCTATGAGCCATGACCCCAATTCGCCCAAGCA	1776	PR	PR	26-JUL-2000; 2000US-0220963P.
QY	1201	TATGGCTCCATTTTAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1260	PR	PR	14-AUG-2000; 2000US-0225266P.
Db	1777	TATGGCTCCATTTTAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1836	PR	PR	14-AUG-2000; 2000US-0225267P.
QY	1261	CCTAGTCCACAGATTCCAGACTGTCTCTCCAGGACCAAGTGGC	1306	PR	PR	14-AUG-2000; 2000US-0225268P.
Db	1837	CCTAGTCCACAGATTCCAGACTGTCTCTCCAGGACCAAGTGGC	1882	PR	PR	14-AUG-2000; 2000US-0225270P.
RESULT 7				PR	PR	14-AUG-2000; 2000US-0225447P.
ABK44021				PR	PR	14-AUG-2000; 2000US-0225575P.
ID	ABK44021	standard; DNA; 2046 BP.		PR	PR	14-AUG-2000; 2000US-0225758P.
AC	ABK44021;			PR	PR	14-AUG-2000; 2000US-0225759P.
XX				PR	PR	18-AUG-2000; 2000US-0226279P.
XX				PR	PR	22-AUG-2000; 2000US-0226681P.
XX				PR	PR	22-AUG-2000; 2000US-0227182P.
DT	05-JUN-2002 (first entry)			PR	PR	23-AUG-2000; 2000US-0227009P.
DE	Genomic DNA encoding novel central nervous system protein #33.			PR	PR	30-AUG-2000; 2000US-0228924P.
KW	Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;			PR	PR	01-SEP-2000; 2000US-0229287P.
KW	hyperproliferative disorder; neoplasm; cardiovascular disorder;			PR	PR	01-SEP-2000; 2000US-0229343P.
KW	cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;			PR	PR	01-SEP-2000; 2000US-0229344P.
KW	nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;			PR	PR	01-SEP-2000; 2000US-0229345P.
KW	acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;			PR	PR	05-SEP-2000; 2000US-0229509P.
KW	adenocarcinoma; reproductive system disorder; testicular feminisation;			PR	PR	05-SEP-2000; 2000US-0229513P.
KW	endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;			PR	PR	06-SEP-2000; 2000US-0230437P.
KW	respiratory disorder; renal disorder; kidney failure; blood disorder;			PR	PR	08-SEP-2000; 2000US-0231242P.
KW	myocardial infarction; wound healing; cell proliferation; skin aging;			PR	PR	08-SEP-2000; 2000US-0231243P.
KW	food additive; food preservative; gene therapy; gene; ds.			PR	PR	08-SEP-2000; 2000US-0231413P.
OS	Homo sapiens.			PR	PR	08-SEP-2000; 2000US-0231414P.
XX				PR	PR	08-SEP-2000; 2000US-0232080P.
XX				PR	PR	12-SEP-2000; 2000US-0231968P.
XX				PR	PR	14-SEP-2000; 2000US-0232397P.
XX				PR	PR	14-SEP-2000; 2000US-0232398P.
XX				PR	PR	14-SEP-2000; 2000US-0232399P.
XX				PR	PR	14-SEP-2000; 2000US-0232400P.
XX				PR	PR	14-SEP-2000; 2000US-0232401P.
XX				PR	PR	14-SEP-2000; 2000US-0233063P.
XX				PR	PR	14-SEP-2000; 2000US-0233064P.
XX				PR	PR	21-SEP-2000; 2000US-0233065P.
XX				PR	PR	21-SEP-2000; 2000US-0234223P.
XX				PR	PR	21-SEP-2000; 2000US-0234274P.
XX				PR	PR	25-SEP-2000; 2000US-0234997P.
XX				PR	PR	25-SEP-2000; 2000US-0234998P.
XX				PR	PR	26-SEP-2000; 2000US-0235484P.
XX				PR	PR	27-SEP-2000; 2000US-0235834P.
XX				PR	PR	27-SEP-2000; 2000US-0235836P.

PR	29-SEP-2000;	2000US-0236327P.	XX	WPI; 2001-581633/65.
PR	29-SEP-2000;	2000US-0236367P.	DR	
PR	29-SEP-2000;	2000US-0236368P.	XX	New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
PR	29-SEP-2000;	2000US-0236369P.	PT	
PR	29-SEP-2000;	2000US-0236370P.	PT	
PR	02-OCT-2000;	2000US-0236802P.	XX	Disclosure; SEQ ID NO 1209; 837pp; English.
PR	02-OCT-2000;	2000US-0237037P.	PS	
PR	02-OCT-2000;	2000US-0237038P.	XX	The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (II) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional
PR	08-NOV-2000;	2000US-0241786P.	CC	
PR	08-NOV-2000;	2000US-0241787P.	CC	
PR	08-NOV-2000;	2000US-0241808P.	CC	
PR	08-NOV-2000;	2000US-0241809P.	CC	
PR	08-NOV-2000;	2000US-0241826P.	CC	
PR	08-NOV-2000;	2000US-024617P.	CC	
PR	08-NOV-2000;	2000US-0246474P.	CC	
PR	08-NOV-2000;	2000US-0246475P.	CC	
PR	08-NOV-2000;	2000US-0246476P.	CC	
PR	08-NOV-2000;	2000US-0246477P.	CC	
PR	08-NOV-2000;	2000US-0246478P.	CC	
PR	08-NOV-2000;	2000US-0246523P.	CC	
PR	08-NOV-2000;	2000US-0246524P.	CC	
PR	08-NOV-2000;	2000US-0246525P.	CC	
PR	08-NOV-2000;	2000US-0246526P.	CC	
PR	08-NOV-2000;	2000US-0246527P.	CC	
PR	08-NOV-2000;	2000US-0246528P.	CC	
PR	08-NOV-2000;	2000US-0246532P.	CC	
PR	08-NOV-2000;	2000US-0246609P.	CC	
PR	08-NOV-2000;	2000US-0246610P.	CC	
PR	08-NOV-2000;	2000US-0246811P.	CC	
PR	08-NOV-2000;	2000US-0246813P.	CC	
PR	17-NOV-2000;	2000US-0249207P.	PR	
PR	17-NOV-2000;	2000US-0249208P.	PR	
PR	17-NOV-2000;	2000US-0249209P.	PR	
PR	17-NOV-2000;	2000US-0249210P.	PR	
PR	17-NOV-2000;	2000US-0249211P.	PR	
PR	17-NOV-2000;	2000US-0249212P.	PR	
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PR	17-NOV-2000;	2000US-0249215P.	PR	
PR	17-NOV-2000;	2000US-0249216P.	PR	
PR	17-NOV-2000;	2000US-0249217P.	PR	
PR	17-NOV-2000;	2000US-0249218P.	PR	
PR	17-NOV-2000;	2000US-0249244P.	PR	
PR	17-NOV-2000;	2000US-0249245P.	PR	
PR	17-NOV-2000;	2000US-0249264P.	PR	
PR	17-NOV-2000;	2000US-0249265P.	PR	
PR	17-NOV-2000;	2000US-0249297P.	PR	
PR	17-NOV-2000;	2000US-0249299P.	PR	
PR	17-NOV-2000;	2000US-0249300P.	PR	
PR	01-DEC-2000;	2000US-0250160P.	PR	
PR	01-DEC-2000;	2000US-0250391P.	PR	
PR	05-DEC-2000;	2000US-0251030P.	PR	
PR	05-DEC-2000;	2000US-0251988P.	PR	
PR	05-DEC-2000;	2000US-0256719P.	PR	
PR	06-DEC-2000;	2000US-0251479P.	PR	
PR	08-DEC-2000;	2000US-0251856P.	PR	
PR	08-DEC-2000;	2000US-0251866P.	PR	
PR	08-DEC-2000;	2000US-0251869P.	PR	
PR	08-DEC-2000;	2000US-0251989P.	PR	
PR	08-DEC-2000;	2000US-0251990P.	PR	
PR	11-DEC-2000;	2000US-0254097P.	PR	
PR	05-JAN-2001;	2001US-0259678P.	PR	
XX				
PA	(HUMA-) HUMAN GENOME SCI INC.			
XX	Rosen CA, Barash SC, Ruben SM;			
PI				

XX Novel polypeptide useful for diagnosis, prognosis, prevention, and
PT treatment of immune, hyperproliferative, renal, respiratory,
PT cardiovascular, reproductive, endocrine, gastrointestinal and
PT neurological disorders.
XX PS Disclosure; Page 296-297; 335pp; English.
XX
CC The invention relates to an isolated polypeptide comprising a sequence at
CC least 90% identical to a full length protein sequence selected from 55
CC sequences given in the specification such as a sequence of 163, 74 or 140
CC amino acids fully defined in the specification, or the encoding sequence
CC contained in 43 cDNA clones given in specification e.g. HCFAT05, HMAE95
CC or HNBW01. The protein and its encoding nucleic acid are useful for
CC diagnosing a pathological condition or susceptibility to a pathological
CC condition in a subject and for preventing, treating or ameliorating a
CC medical condition. The protein, its encoding nucleic acid and an isolated
CC antibody that can bind to the protein are useful in treating, preventing,
CC diagnosing and/or prognosing immunodeficiencies, autoimmune disorders,
CC allergic reactions and conditions, inflammatory conditions, graft-versus-
CC host disease, blood-related disorders, hyperproliferative disorders,
CC renal disorders, cardiovascular disorders, respiratory disorders,
CC neurological disorders, endocrine disorders, reproductive system
CC disorders, infectious diseases, and gastrointestinal disorders. The
CC protein of the invention is useful to stimulate neuronal growth and to
CC treat, prevent, and/or diagnose neuronal damage which occurs in certain
CC neuronal disorders or neuro-degenerative conditions, for stimulating
CC keratinocyte growth, to prevent hair loss, to modulate mammalian
CC characteristics such as body height, weight, hair color, and to increase
CC or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors or other nutritional
CC components. The nucleic acid of the invention can be used in gene
CC therapy. This polynucleotide sequence represents one of the novel nucleic
CC acids of the invention
XX
SQ Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;
Query Match 99.6%; Score 1306; DB 6; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATGCTAGGTTCTGATTCCTCTTCTTCCACCTCTGCTCTTTAGGCTCTATC 60
DB 577 TTGAATGCTAGGTTCTGATTCCTCTTCTTCCACCTCTGCTCTTTAGGCTCTATC 636
QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCTGTACATGATGCTGTGGGCTATCGT 120
DB 637 ATGTGGAACAGCTCTGACGCCAACTTCTCTGTACATGATGCTGTGGGCTATCGT 696
QY 121 TATGTTGCAAGTTAGCTGGGGGGTGGTGGTGTGACAGGACCGGTGGGCAATGTGCTC 180
DB 697 TATGTTGCAAGTTAGCTGGGGGGTGGTGGTGTGACAGGACCGGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTATAGCC 240
DB 757 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTATAGCC 816
QY 241 AACCTCACATGGCTGATCTCTTACTGACAGCTCCTTTCAGCCCTTCTCTGTGGACAC 300
DB 817 AACCTCACATGGCTGATCTCTTACTGACAGCTCCTTTCAGCCCTTCTCTGTGGACAC 876
QY 301 TACCTCCACCTGACCTGGGCGACCGGTGGCACTTCTGACAGGATATTTGGGCTCCTCTT 360
DB 877 TACCTCCACCTGACCTGGGCGACCGGTGGCACTTCTGACAGGATATTTGGGCTCCTCTT 936
QY 361 TTGGCTTCCAAATTTCTGCTCATCTGACCTCTGCTCATGCTGACCTGGGAGCTACCTTC 420
DB 937 TTGGCTTCCAAATTTCTGCTCATCTGACCTCTGCTCATGCTGACCTGGGAGCTACCTTC 996
QY 421 CTCATTGCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 480
DB 997 CTCATTGCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 1056

QY 481 CTGTTGAGCACTTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 540
DB 1057 CTGTTGAGCACTTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 1116
QY 541 CTGTTACTCTGTAGTCTGACCTGTCAGCTTTGACCGCATCCGAGCCGCGCTTACACCA 600
DB 1117 CTGTTACTCTGTAGTCTGACCTGTCAGCTTTGACCGCATCCGAGCCGCGCTTACACCA 1176
QY 601 ATCTCATGGGCATCTACTTTGTGTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 660
DB 1177 ATCTCATGGGCATCTACTTTGTGTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
QY 561 ATCCACCGCCAGGTTCAACGAGCAGCAGCAGCAGTGCACCAATACAAAGTTGCGCAGCA 720
DB 1237 ATCCACCGCCAGGTTCAACGAGCAGCAGCAGTGCACCAATACAAAGTTGCGCAGCA 1286
QY 721 AGCATCCACTCCAAACCACTGTGGCCAGGACTGATGAGGCCATGCTGCTGCTTCCAGG 780
DB 1297 AGCATCCACTCCAAACCACTGTGGCCAGGACTGATGAGGCCATGCTGCTGCTTCCAGG 1356
QY 781 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 840
DB 1357 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 1416
QY 841 GCTGCCACCCAGCAGCAGCAGGAGGAGTCTCATCAGAGTGGGAGACCAAGATCAACAGC 900
DB 1417 GCTGCCACCCAGCAGCAGCAGGAGGAGTCTCATCAGAGTGGGAGACCAAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGCCAGCCCA 960
DB 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGCCAGCCCA 1536
QY 961 ATTTAAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAAGTGTGACTCGA 1020
DB 1537 ATTTAAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAAGTGTGACTCGA 1596
QY 1021 TGTGTTGCTGTGTTCTCTGCTTTGCTTGGCTGAGCTACATCCCTTCTTCTGCTCAACAT 1080
DB 1597 TGTGTTGCTGTGTTCTCTGCTTTGCTTGGCTGAGCTACATCCCTTCTTCTGCTCAACAT 1656
QY 1081 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCACCTCACCTGG 1140
DB 1657 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCACCTCACCTGG 1716
QY 1141 CTCATAGTGTTCATCAACCCCTGTCTCTATGACGCCATGAACCCCAATTCGGCCAAAGCA 1200
DB 1717 CTCATAGTGTTCATCAACCCCTGTCTCTATGACGCCATGAACCCCAATTCGGCCAAAGCA 1776
QY 1201 TATGGCTCCATTTTAAAGAGAGGCGCCGGAGTTTCCATAGGCTCCATTTAGAACTGTGAC 1260
DB 1777 TATGGCTCCATTTTAAAGAGAGGCGCCGGAGTTTCCATAGGCTCCATTTAGAACTGTGAC 1836
QY 1261 CCTAGTCACCAAGATTCAGGACTGCTCTCCAGGACCAAGTGGC 1306
DB 1837 CCTAGTCACCAAGATTCAGGACTGCTCTCCAGGACCAAGTGGC 1882

RESULT 10
ABV84126
ID ABV84126 standard; DNA; 2046 BP.
XX
AC ABV84126;
XX
XX 09-DEC-2002 (first entry)
XX
XX Human polynucleotide SEQ ID NO 875.
DE
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antiskinning; antianemic; antitubercular; cancer;
KW antineumatic; hepatotropic; cerebroprotective; anti-inflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;

KW	neurological disease; infection; nephrotropic; gene therapy; vaccine;	PT	neurological disorders.
KW	gene; ds.	XX	Disclosure; SEQ ID NO 875; 369pp + Sequence Listing; English.
XX	Homo sapiens.	XX	The invention relates to novel genes (ABV83682-ABV84101) and proteins
OS		CC	(ABP6710-ABP67129) useful for preventing, treating or ameliorating
PN	US2002090672-A1.	CC	medical conditions e.g. by protein or gene therapy. The genes are
XX	11-JUL-2002.	CC	isolated from a range of human tissues disclosed in the specification.
PD		CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX	17-JAN-2001; 2001US-00764853.	CC	the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
PR	31-JAN-2000; 2000US-0179065P.	CC	ovarian cancer, and other cancers of the adrenal gland, bone, marrow,
PR	04-FEB-2000; 2000US-0180628P.	CC	breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
PR	28-JUN-2000; 2000US-0214886P.	CC	disorders e.g. Addison's disease, allergies, autoimmune haemolytic
PR	07-JUL-2000; 2000US-0216647P.	CC	anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
PR	07-JUL-2000; 2000US-0216880P.	CC	multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
PR	11-JUL-2000; 2000US-0217487P.	CC	cardiovascular disorders such as myocardial ischaemia; (d) wound healing
PR	14-JUL-2000; 2000US-0217486P.	CC	; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
PR	14-JUL-2000; 2000US-0218290P.	CC	infectious diseases such as viral, bacterial, fungal and parasitic
PR	26-JUL-2000; 2000US-0220963P.	CC	infections. Note: The sequence data for this patent did not form part of
PR	14-AUG-2000; 2000US-0220964P.	CC	the printed specification, but was obtained in electronic format directly
PR	14-AUG-2000; 2000US-0224518P.	XX	from WIPO at ftp.wipo.int/pub/published_pct_sequences
PR	14-AUG-2000; 2000US-0224519P.	SQ	Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;
PR	14-AUG-2000; 2000US-0225267P.		
PR	14-AUG-2000; 2000US-0225268P.		
PR	14-AUG-2000; 2000US-0225270P.		
PR	14-AUG-2000; 2000US-0225447P.		
PR	14-AUG-2000; 2000US-0225757P.		
PR	22-AUG-2000; 2000US-0225758P.		
PR	30-AUG-2000; 2000US-0228924P.		
PR	01-SEP-2000; 2000US-0229287P.		
PR	01-SEP-2000; 2000US-0229343P.		
PR	01-SEP-2000; 2000US-0229344P.		
PR	01-SEP-2000; 2000US-0229345P.		
PR	05-SEP-2000; 2000US-0229509P.		
PR	05-SEP-2000; 2000US-0229513P.		
PR	08-SEP-2000; 2000US-0231413P.		
PR	21-SEP-2000; 2000US-0234223P.		
PR	21-SEP-2000; 2000US-0234274P.		
PR	25-SEP-2000; 2000US-0234977P.		
PR	27-SEP-2000; 2000US-0235834P.		
PR	29-SEP-2000; 2000US-0236377P.		
PR	29-SEP-2000; 2000US-0236378P.		
PR	29-SEP-2000; 2000US-0236386P.		
PR	29-SEP-2000; 2000US-0236389P.		
PR	29-SEP-2000; 2000US-0236370P.		
PR	02-OCT-2000; 2000US-0236802P.		
PR	02-OCT-2000; 2000US-0237037P.		
PR	02-OCT-2000; 2000US-0237038P.		
PR	02-OCT-2000; 2000US-0237039P.		
PR	02-OCT-2000; 2000US-0237040P.		
PR	13-OCT-2000; 2000US-0239935P.		
PR	20-OCT-2000; 2000US-0240960P.		
PR	20-OCT-2000; 2000US-0241785P.		
PR	20-OCT-2000; 2000US-0241809P.		
PR	01-NOV-2000; 2000US-0244617P.		
PR	17-NOV-2000; 2000US-0249299P.		
PR	08-DEC-2000; 2000US-0251856P.		
PR	08-DEC-2000; 2000US-0251868P.		
PR	08-DEC-2000; 2000US-0251869P.		
XX	(ROSE/) ROSEN C A.		
PA	(RUBE/) RUBEN S M.		
PA	(BARA/) BARASH S C.		
XX	Rosen CA, Ruben SM, Barash SC;		
FI	WPI; 2002-681727/73.		
XX	Novel polypeptide useful for diagnosis, prognosis, prevention, and		
DR	treatment of immune, hyperproliferative, renal, respiratory,		
XX	cardiovascular, reproductive, endocrine, gastrointestinal and		
PT			
PT			

[illegible]

PR	02-OCT-2000;	2000US-0237040P.	PT	or disorders.
PR	13-OCT-2000;	2000US-0239335P.	XX	Disclosure; Page 308-309; 363pp; English.
PR	13-OCT-2000;	2000US-0239337P.	XX	The invention relates to isolated nucleic acids encoding novel
PR	20-OCT-2000;	2000US-0240960P.	XX	polypeptides. The nucleic acids are useful for chromosome mapping, for
PR	20-OCT-2000;	2000US-0241221P.	CC	radiation hybrid mapping, for detection of cancer, in gene therapy, for
PR	20-OCT-2000;	2000US-0241785P.	CC	identifying individuals from minute biological samples, as an alternative
PR	20-OCT-2000;	2000US-0241786P.	CC	to restriction fragment length polymorphism (RFLP) analysis, in forensic
PR	20-OCT-2000;	2000US-0241787P.	CC	biology and as hybridisation probes for differential identification of
PR	20-OCT-2000;	2000US-0241808P.	CC	tissues or cell types present in a biological sample. Compositions
PR	20-OCT-2000;	2000US-0241809P.	CC	comprising the polynucleotides, polypeptides and antibodies specific for
PR	20-OCT-2000;	2000US-0241826P.	CC	the polypeptides may be used in the diagnosis, prognosis, prevention
PR	01-NOV-2000;	2000US-0244617P.	CC	and/or treatment of kidney disorders (e.g. glomerulonephritis, urinary
PR	08-NOV-2000;	2000US-0246474P.	CC	tract infections, chronic nephritis), cardiovascular disorders (e.g.
PR	08-NOV-2000;	2000US-0246475P.	CC	arrhythmias, carotid heart disease, endocarditis), blood disorders
PR	08-NOV-2000;	2000US-0246477P.	CC	(e.g. thrombosis, anaemia, haemoglobin abnormalities), electrolyte
PR	08-NOV-2000;	2000US-0246478P.	CC	imbalance, neoplastic disorders (e.g. cancers), respiratory disorders
PR	08-NOV-2000;	2000US-0246523P.	CC	(e.g. acute rhinitis, sinusitis, pharyngitis) and neurological disorders
PR	08-NOV-2000;	2000US-0246524P.	CC	(e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease).
PR	08-NOV-2000;	2000US-0246525P.	CC	Sequences ACD01492-ACD01506 represent human genomic DNA molecules of the
PR	08-NOV-2000;	2000US-0246526P.	CC	invention
PR	08-NOV-2000;	2000US-0246527P.	XX	Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;
PR	08-NOV-2000;	2000US-0246528P.	XX	Query Match 99.6%; Score 1306; DB 7; Length 2046;
PR	08-NOV-2000;	2000US-0246529P.	XX	Best Local Similarity 100.0%; Pred. No. 0;
PR	17-NOV-2000;	2000US-0249207P.	XX	Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	17-NOV-2000;	2000US-0249208P.	QY	1 TTGAATGCTAGTTCGTGATTCCTCTTCTTCCACCTCTGCTCTTTAGCCTCTATC 60
PR	17-NOV-2000;	2000US-0249209P.	Db	577 TTGAATGCTAGTTCGTGATTCCTCTTCTTCCACCTCTGCTCTTTAGCCTCTATC 636
PR	17-NOV-2000;	2000US-0249210P.	QY	61 ATGTGGAACAGCTCTGACGCCAATCTCTCTGCTACCATGATCTGTCTGGGTATCGT 120
PR	17-NOV-2000;	2000US-0249211P.	Db	637 ATGTGGAACAGCTCTGACGCCAATCTCTCTGCTACCATGATCTGTCTGGGTATCGT 696
PR	17-NOV-2000;	2000US-0249212P.	QY	121 TATGTTGAGTTCGTGGGGGTGCTGCTGTGTGACAGGACCGTGGGCAATGTGCTC 180
PR	17-NOV-2000;	2000US-0249213P.	Db	697 TATGTTGAGTTCGTGGGGGTGCTGCTGTGTGACAGGACCGTGGGCAATGTGCTC 756
PR	17-NOV-2000;	2000US-0249214P.	QY	181 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGCTCATAGCC 240
PR	17-NOV-2000;	2000US-0249215P.	Db	757 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGCTCATAGCC 816
PR	17-NOV-2000;	2000US-0249216P.	QY	241 AACCTCACACATGGCTGATCTCTCTACTGACGCTCTTTCAGCCCTTCTCTGTGGACAC 300
PR	17-NOV-2000;	2000US-0249217P.	Db	817 AACCTCACACATGGCTGATCTCTCTACTGACGCTCTTTCAGCCCTTCTCTGTGGACAC 876
PR	17-NOV-2000;	2000US-0249218P.	QY	301 TACTTCCACCTGACATGGCCGACCGGTGCCACCTTCTGACGGGTATTTGGGCTCTCTCTT 360
PR	17-NOV-2000;	2000US-0249219P.	Db	877 TACTTCCACCTGACATGGCCGACCGGTGCCACCTTCTGACGGGTATTTGGGCTCTCTCTT 936
PR	17-NOV-2000;	2000US-0249220P.	QY	361 TTTGGCTCCAAATCTGCTCCATCTGACCTCTGCTGACCTCATCGGACCTGGGACGCTACCTC 420
PR	17-NOV-2000;	2000US-0249221P.	Db	937 TTTGGCTCCAAATCTGCTCCATCTGACCTCTGCTGACCTCATCGGACCTGGGACGCTACCTC 996
PR	17-NOV-2000;	2000US-0249222P.	QY	421 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGTGCAAGGGGATAGTCTGGCA 480
PR	17-NOV-2000;	2000US-0249223P.	Db	997 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGTGCAAGGGGATAGTCTGGCA 1056
PR	17-NOV-2000;	2000US-0249224P.	QY	481 CTGGTGACACCTGGGTTGTGGGGTGGCCAGCTTGTCTCCCTCTGGCTTATTTATC 540
PR	17-NOV-2000;	2000US-0249225P.	Db	1057 CTGGTGACACCTGGGTTGTGGGGTGGCCAGCTTGTCTCCCTCTGGCTTATTTATC 1116
PR	17-NOV-2000;	2000US-0249226P.	QY	541 CTGGTACCTGTAGTCTGCACCTGACCTTTTTCAGCGCATCCGAGCCCGGCTTACACCA 600
PR	17-NOV-2000;	2000US-0249227P.	Db	1117 CTGGTACCTGTAGTCTGCACCTGACCTTTTTCAGCGCATCCGAGCCCGGCTTACACCA 1176
PR	17-NOV-2000;	2000US-0249228P.	QY	601 ATCTCATGGGCATCTACTTTTGTCTGGGCTGACAGTGTGGCATCTTCTATTGCTC 660
PR	17-NOV-2000;	2000US-0249229P.	Db	1177 ATCTCATGGGCATCTACTTTTGTCTGGGCTGACAGTGTGGCATCTTCTATTGCTC 1236

XX (ROSE/) ROSEN C A.
 FA (RUBE/) RUBEN S M.
 FA (BARA/) BARASH S C.
 XX Rosen CA, Ruben SM, Barash SC;
 PI WPI; 2003-416807/39.
 DR New nucleic acids and polypeptides, useful for diagnosing, prognosing,
 XX preventing and/or treating e.g. kidney, cardiovascular, blood,
 PT electrolyte imbalance, neoplastic, respiratory, or neurological diseases
 PT

Qy	661	ATCCACGCCAGGTCAAAACGACGACGACGACCTGGACCAATACAAAGTTGGCAGGCCA	720
Db	1237	ATCCACGCCAGGTCAAAACGACGACGACGACCTGGACCAATACAAAGTTGGCAGGCCA	1296
Qy	721	AGCATCCACTCCAAACCATGTGGCCAGGACATGATGAGGCCATGCTGGTTCGTTCCAGGAG	780
Db	1297	AGCATCCACTCCAAACCATGTGGCCAGGACATGATGAGGCCATGCTGGTTCGTTCCAGGAG	1356
Qy	781	CTGACACGCGAGTTAGCATCAGGAGGACCCAGATGAGGGGATTTCACTGAGCCAGTCAGT	840
Db	1357	CTGACACGCGAGTTAGCATCAGGAGGACCCAGATGAGGGGATTTCACTGAGCCAGTCAGT	1416
Qy	841	GCTGCCACCCACGAGACCCCTGGAAAGGGGATCATCAAGATGGGAGACCAAGATCAACAGC	900
Db	1417	GCTGCCACCCACGAGACCCCTGGAAAGGGGATCATCAAGATGGGAGACCAAGATCAACAGC	1476
Qy	901	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAAGCCA	960
Db	1477	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAAGCCA	1536
Qy	961	ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAGGTGACTCGAATG	1020
Db	1537	ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAGGTGACTCGAATG	1596
Qy	1021	TGTTTTGCTGTGTTCTCTGCTTTGCCCTCAGCTACATCCCTCTTTGCTGCTCAACATT	1080
Db	1597	TGTTTTGCTGTGTTCTCTGCTTTGCCCTCAGCTACATCCCTCTTTGCTGCTCAACATT	1656
Qy	1081	CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCAACCTCACTGG	1140
Db	1657	CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCAACCTCACTGG	1716
Qy	1141	CTCAATGGTTGTCATCAACCTGTGCTCTATGACGACCATGAACGCCCAATTCGCCCAAGCA	1200
Db	1717	CTCAATGGTTGTCATCAACCTGTGCTCTATGACGACCATGAACGCCCAATTCGCCCAAGCA	1776
Qy	1201	TATGGCTCCATTTTAAAGAGGAGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1260
Db	1777	TATGGCTCCATTTTAAAGAGGAGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1836
Qy	1261	CCTAGTCACAGAAATTCAGGACTGTCTCCTCCAGGACCAAAGTGGC	1306
Db	1837	CCTAGTCACAGAAATTCAGGACTGTCTCCTCCAGGACCAAAGTGGC	1882
RESULT	12		
AD46506			
ID	AD46506	standard; DNA; 2046 bp.	
XX	AC	AD46506;	
XX	DT	18-DEC-2003 (first entry)	
XX	DE	Human neoplastic disease-associated gene 16 DNA #1.	
XX	KW	Neoplastic disease-associated polypeptide; gene therapy;	
XX	KW	hyperproliferative disease; cancer; autoimmune disorder; diabetes;	
XX	KW	rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;	
XX	KW	autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;	
XX	KW	haematologic disorder; anaemia; thrombocytopoenia; allergic reaction;	
XX	KW	asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;	
XX	KW	inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;	
XX	KW	Alzheimer's disease; Parkinson's disease; renal disorder;	
XX	KW	acute glomerulonephritis; end-stage renal disease;	
XX	KW	cardiovascular disorder; atherosclerosis; myocarditis;	
XX	KW	infectious disease; AIDS; cachexia; anorexia; wound healing;	
XX	KW	epithelial cell proliferation; Human; ds.	
OS		Homo sapiens.	
XX	FN	US2003082758-A1.	
XX	PD	01-MAY-2003.	

29-SEP-2000;	2000US-0236369P.	XX	New isolated human neoplastic disease-associated polypeptides and
29-SEP-2000;	2000US-0236370P.	PT	poly nucleotides, useful for diagnosing, preventing, prognosticating or
02-OCT-2000;	2000US-0236802P.	PT	treatment of medical conditions such as cancer, AIDS, diabetes or Parkinson's
02-OCT-2000;	2000US-0237037P.	PT	disease.
02-OCT-2000;	2000US-0237038P.	XX	Disclosure; SEQ ID NO 592; 302pp; English.
02-OCT-2000;	2000US-0237039P.	XX	The invention relates to one of 238 disclosed human neoplastic disease-
02-OCT-2000;	2000US-0237040P.	XX	associated polypeptides encoded by 171 disclosed cDNA sequences
13-OCT-2000;	2000US-0239335P.	CC	(including their domains, epitopes, full-length proteins, allelic variants
20-OCT-2000;	2000US-0240960P.	CC	or species homologues). Also included are those encoding nucleic acids, a
20-OCT-2000;	2000US-0241221P.	CC	recombinant vector comprising the nucleic acid, a recombinant host cell
20-OCT-2000;	2000US-0241786P.	CC	comprising the nucleic acid (expressing the protein), an isolated
20-OCT-2000;	2000US-0241787P.	CC	antibody that binds specifically to the isolated polypeptide, preventing,
20-OCT-2000;	2000US-0241808P.	CC	treatment or ameliorating a medical condition, diagnosing a pathological
20-OCT-2000;	2000US-0241809P.	CC	condition or a susceptibility to a pathological condition in a subject,
20-OCT-2000;	2000US-0241826P.	CC	identifying a binding partner to the polypeptide, identifying an activity
01-NOV-2000;	2000US-0244617P.	CC	in a biological assay, and the gene corresponding to the cDNA sequence.
08-NOV-2000;	2000US-0246474P.	CC	The polypeptides, polynucleotides and antibodies are useful for
08-NOV-2000;	2000US-0246475P.	CC	detecting, preventing, diagnosing, prognosticating, treating or
08-NOV-2000;	2000US-0246476P.	CC	ameliorating medical conditions such as hyperproliferative diseases or
08-NOV-2000;	2000US-0246477P.	CC	cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
08-NOV-2000;	2000US-0246478P.	CC	systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
08-NOV-2000;	2000US-0246523P.	CC	or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
08-NOV-2000;	2000US-0246524P.	CC	anaemia or thrombocytopenia), allergic reactions including asthma or
08-NOV-2000;	2000US-0246525P.	CC	eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
08-NOV-2000;	2000US-0246526P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
08-NOV-2000;	2000US-0246527P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
08-NOV-2000;	2000US-0246528P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
08-NOV-2000;	2000US-0246529P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
08-NOV-2000;	2000US-0246532P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
08-NOV-2000;	2000US-0246533P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
08-NOV-2000;	2000US-0246609P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
08-NOV-2000;	2000US-0246610P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
08-NOV-2000;	2000US-0246611P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
08-NOV-2000;	2000US-0246613P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249207P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249208P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249209P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249210P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249211P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249212P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249213P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249214P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249215P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249216P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249217P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
17-NOV-2000;	2000US-0249218P.	CC	inflammatory bowel disease or Crohn's disease), neurodegenerative
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Qy	829	GAGCGATCATGTGTGCGCACACCCAGACCGCTGGAAAGGGGACTCATCAGAAGTGGGAGAC	888
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Qy	889	CAGATCAACAGCAGAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCAGAAAGCATCTGCC	948
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Qy	949	AAAGCCCGAGCCAATTAAAGGAGCCAGAAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAG	1008
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Qy	1009	GTGACTCGAATGTGTTTTGTGTGTTTCCCTCTGCTTTTGCCCTGAGCTACATCCCTTCTTG	1068
Db	1024	GTGACTCGAATGTGTTTTGTGTGTTTCCCTCTGCTTTTGCCCTGAGCTACATCCCTTCTTG	1083
Qy	1069	CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGTCTGCC	1128
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Qy	1189	TTCCGCCAAGCATATGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT	1248
Db	1204	TTCCGCCAAGCATATGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT	1263
Qy	1249	TAGAACTGTGACCCCTAGTCCACCAAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC	1306
Db	1264	TAGAACTGTGACCCCTAGTCCACCAAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC	1321

RESULT 15

RESULT IS
AAS98070
ID AAS98070 standard: DNA: 1546 BP.

XX
AC
AAS98070:AC
XX
AAS98070;

DT 12-MAR-2002 (first entry)

DI 12-MAR-2002 (LIST ENCLY)
XX

Human DNA for potential G protein-coupled receptor #27.

Human; G protein-coupled receptor; GPCR; ds; GAI4; galanin receptor;
 Alzheimer's disease; amyotrophic lateral sclerosis; aschma;
 Atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;
 chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
 depression; epilepsy; macular degeneration; lymphoma; melanoma;
 multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
 psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
 tuberculosis; cognition disorder; memory disorder; anorexia;
 hormonal release disorder; cardiovascular activity disorder;

KW	pain perception disorder; obesity; diabetes; obesity; diabetes;
KW	hyperlipidaemia; stroke; gene therapy.
XX	
OS	Homo sapiens.
XX	
XX	W02000185791-A1.
XX	
XX	15-NOV-2001.
PD	
XX	
XX	11-MAY-2001; 2001WO-US015332.
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XX	11-MAY-2000; 2000US-0203217P.
PR	
PR	18-MAY-2000; 2000US-0205945P.
XX	
XX	(LIFE-) LIFESPAN BIOSCIENCES INC.
PA	
XX	
XX	Brown JP, Miller M, Burner G, Fabre-Suver C, Pritchard D;
PI	
XX	WPI; 2002-066595/09.
XX	
DR	
XX	
PT	Novel G protein-coupled receptor polypeptides including galanin receptor
PT	polypeptides useful for identifying modulators that are useful for
PT	treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,
PT	stroke.
PT	

XX
PS Disclosure: Page 130-131; 144pp; English.

The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequences (including antisense probes), a host cell comprising an expression vector comprising the GPCR sequence, antibodies raised against the polypeptides, and methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds which function as modulators, activators, repressors, agonists or antagonists of the novel GPCR polypeptides including the GAL4 polypeptide. The antibodies and nucleic acid probes as described above can be used to detect the presence of the polypeptides and nucleic acids and are used to diagnose a variety of diseases or disorders in which GPCRs are involved e.g., Alzheimer's disease, amyotrophic lateral sclerosis, asthma, atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease, depression, epilepsy, macular degeneration, lymphoma, melanoma, multiple sclerosis, osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory disorders, anorexia, hormonal release disorders, cardiovascular activity disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polynucleotide of the invention.

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SQ Sequence 1546 BP: 383 A: 442 C: 351 G: 370 T: 0 U: 0 Other:

Query Match	95.8%	Score 1256.4	DB 6	Length 1546
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Query Macchi 93.8%; score 1230.4; length 1310
Best Local Similarity 99.9%; Pred. No. 0;

Best Local Similarity 99.9%, Freq. NO: 0,
Matches 1257: Conservative 0; Mismatches 1; Indels 0;

MARCOONES TESS /
CORRECTIONAL
INFORMATION
S - / MARCOON
MARCOON

QY 49 TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAG

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109	CTGGGCTATCGTTATGTTGCAGTTAGCTGTGGGGGTGGTGGTGGCTGCACAGGCCCGTG	Qy
139	CTGGGCTATCGTTATGTTGCAGTTAGCTGTGGGGGTGGTGGTGGCTGCACAGGCCCGTG	Db
169	GGCAATGTGTCACCCCTACTGGCCTTTGGCCATCCAGGCCCAAGCTCCGTACCGGATTCAC	Qy
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Job time : 596.574 secs

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Qy	349	GGGCTCTCTCTTTTGGCTCCAAATTCGTGTCTCAATTCCTGACCTCTGCTGCTCATCGCACTG	408
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Qy	409	GGAGCTTACCTCTCTATTGGCCACCCTTAAGCTTTTTCGCCCAAGTTTTCAGTGCCCAAGGGG	468
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Qy	529	CCATTTTATATCTCTGGTACCTGTAGTCTGCACCTCTGCAGCTTTTGACCCCATCCGAGGCGGG	588
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Qy	589	CTTTACACCACTCTCTCATCTGGGATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATC	648
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Qy	649	TTCTATTTCCTCATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCCAATACAAG	708
Db	679	TTCTATTTCCTCATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCCAATACAAG	738
Qy	709	TTGGCAGAGGAGCATTCCTCAACCATGTGGCCAGGACTGATGAGGCCATGCTCGT	768
Db	739	TTGGCAGAGGAGCATTCCTCAACCATGTGGCCAGGACTGATGAGGCCATGCTCGT	798
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Qy	1009	GTGACTCGAATGTGTTTGTGTGTCTCTCTGTCTTTCCTCTGAGCTACATCCCTCTCTTG	1068
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Qy	1129	AACTCACCCTGGCTCAATGGTTGCATCAACCCCTGTGTCTATGACGCCATGAACCCGCAA	1188
Db	1159	AACTCACCCTGGCTCAATGGTTGCATCAACCCCTGTGTCTATGACGCCATGAACCCGCAA	1218
Qy	1189	TTCCGCCCAAGCATATGGCTCCATTTTAAAGAGGGGCCCGGGAGTTTCCATAGGCTCCAT	1248
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Qy	1249	TAGAACTGTCACTAGTCAACGAATTCAGGACTGTCTCTCCAGGACCAAGTGGC	1306
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GenCore version 5.1.6
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Run on: September 24, 2004, 02:47:20 ; Search time 1055.3 Seconds
(without alignments)
6292.206 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 6674772

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1306	99.6	2046	13	US-09-764-893-130
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10	1256.4	95.8	1498	9	US-09-826-508-37
11	1256.4	95.8	1546	15	US-10-225-567A-584
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13	1256.6	95.8	1579	15	US-10-073-885-11
14	1191	90.8	1191	13	US-10-343-650A-45

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16	887.6	67.7	1191	15	US-10-094-417-21	Sequence 21, Appl
17	754	57.5	1333	15	US-10-017-161-1921	Sequence 1321, A
18	525	40.0	525	15	US-10-029-386-12527	Sequence 13527, A
19	360.4	27.5	485	16	US-10-264-237-348	Sequence 348, App
20	355	27.1	483	9	US-09-764-853-62	Sequence 62, Appl
21	355	27.1	483	10	US-09-989-442-13	Sequence 13, Appl
22	355	27.1	483	10	US-09-764-886-26	Sequence 26, Appl
23	355	27.1	483	11	US-09-764-875-43	Sequence 43, Appl
24	355	27.1	483	13	US-09-764-886-26	Sequence 26, Appl
25	355	27.1	483	13	US-09-764-893-14	Sequence 14, Appl
26	355	27.1	483	15	US-10-073-865-14	Sequence 14, Appl
27	355	27.1	483	15	US-10-103-313-26	Sequence 26, Appl
28	355	27.1	483	15	US-10-073-885-38	Sequence 38, Appl
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45	76.6	5.8	2048	14	US-10-052-589-1	Sequence 1, Appli

ALIGNMENTS

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; APPLICANT: Smith, Kelli E.
; APPLICANT: Weinsbank, Richard L.
; TITLE OF INVENTION: DNA Encoding A Human Receptor (hplsa) And Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 55180
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US/09/179,798A
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
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; ORGANISM: Homo sapiens
US-10-029-436-1

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/ PRIOR APPLICATION NUMBER: 60/232,399
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: 60/232,401
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: 60/241,808
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/241,826
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/241,786
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/241,221
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/246,475
/ PRIOR FILING DATE: 2000-11-08
/ PRIOR APPLICATION NUMBER: 60/231,243
/ PRIOR FILING DATE: 2000-09-08
/ PRIOR APPLICATION NUMBER: 60/233,065
/ PRIOR FILING DATE: 2000-09-14

Query Match          99.6%; Score 1306; DB 10; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATGCTAGGTTCTGATTCCTCTTCCCTCTTCCACCTCTGCTCTTTAGCCTCTATC 60
DB 577 TTGAATGCTAGGTTCTGATTCCTCTTCCCTCTTCCACCTCTGCTCTTTAGCCTCTATC 636
QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTCTGGGTATCGT 120
DB 637 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTCTGGGTATCGT 696
QY 121 TATGTTGCACTAGTCTGGGGGTGGTGGTGTGCTGTGACAGCACCGTGGGCAATGTGCTC 180
DB 697 TATGTTGCACTAGTCTGGGGGTGGTGGTGTGCTGTGACAGCACCGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTCTCTCATAGCC 240
DB 757 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTCTCTCATAGCC 816
QY 241 AACCTCACTGGGTGATCTCTCTATGCAAGCTCTCTTACGCCCTTCTGTGTGGACACC 300
DB 817 AACCTCACTGGGTGATCTCTCTATGCAAGCTCTCTTACGCCCTTCTGTGTGGACACC 876
QY 301 TACCTCCACCTGCATGGCGCACCGGTGCCACCTTCTGACGGGTATTTGGGCTCTCTCTT 360
DB 877 TACCTCCACCTGCATGGCGCACCGGTGCCACCTTCTGACGGGTATTTGGGCTCTCTCTT 936
QY 361 TTTGGCTCCAAATTTGTTCTCCATCTGACCTCTGCTCTCATGCACTGGGACGTACCTC 420
DB 937 TTTGGCTCCAAATTTGTTCTCCATCTGACCTCTGCTCTCATGCACTGGGACGTACCTC 996
QY 421 CTCATTGGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTCTGGCA 480
DB 997 CTCATTGGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTCTGGCA 1056
QY 481 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTGTCTCCCTCTGSCCTATTATATC 540
DB 1057 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTGTCTCCCTCTGSCCTATTATATC 1116
QY 541 CTGGTACCTGTAGTCTGCACCTGTGAGCTTTTACCGCATCCGAGCGGCTTACACACC 600
DB 1117 CTGGTACCTGTAGTCTGCACCTGTGAGCTTTTACCGCATCCGAGCGGCTTACACACC 1176
QY 601 ATCCTCATGGGCATCTACTTTGTGCTGGGCTGACAGTGTGGCATCTTCTATTGCTC 660
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	Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches	0; Indels	0; Gaps	0;
	Matches	1306;	Conservative	0;			
Qy	1	TTGAATGCTAGGTTCGATTCCCTCTTCCCTCTTCCACCCCTCGCCTTTAGCCTCTATC	60				
Dd	1470	TTGAATGCTAGGTTCGATTCCCTCTTCCCTCTTCCACCCCTCGCCTTTAGCCTCTATC	1411				
Qy	61	ATGTGGAAACAGCTCTGACGCCAATTTCTCTGCTACCATGAGTCTGTGCTGGCGTATCGT	120				
Dd	1410	ATGTGGAAACAGCTCTGACGCCAATTTCTCTGCTACCATGAGTCTGTGCTGGCGTATCGT	1351				
Qy	121	TATGTTGCAGTTAGCTGGGGGGTGTTGGTGGCTGTGACAGCACCGTGGGCAATGTGCTC	180				
Dd	1350	TATGTTGCAGTTAGCTGGGGGGTGTTGGTGGCTGTGACAGCACCGTGGGCAATGTGCTC	1291				
Qy	181	ACCTTAATGGCCTTGGCCATCCAGCCCAAAGCTCCGTTACCCGATTCAACTGCTCATAGCC	240				
Dd	1290	ACCCTAATGGCCTTGGCCATCCAGCCCAAAGCTCCGTTACCCGATTCAACTGCTCATAGCC	1231				
Qy	241	AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTCTCTCTGTGGACAC	300				
Dd	1230	AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTCTCTCTGTGGACAC	1171				
Qy	301	TACTCCACCTGCACCTGGCGACCGGTGCCACCTTCTGCAGGGTATTTTGGGCTCCTCCTT	360				
Dd	1170	TACTCCACCTGCACCTGGCGACCGGTGCCACCTTCTGCAGGGTATTTTGGGCTCCTCCTT	1111				
Qy	361	TTTGGCTCCGAATCTGTCTCCATCTGACCCCTGCGCTCATCGCACTGGGAGCGTACCTC	420				
Dd	1110	TTTGGCTCCGAATCTGTCTCCATCTGACCCCTGCGCTCATCGCACTGGGAGCGTACCTC	1051				
Qy	421	CTCATTTGCCACCCCTAAGCTTTTTTCCCACAAAGTTTTCAGTCCCAAGGGGATAGTCTGGCA	480				
Dd	1050	CTCATTTGCCACCCCTAAGCTTTTTTCCCACAAAGTTTTCAGTCCCAAGGGGATAGTCTGGCA	991				
Qy	481	CTGGTAGACACTGGGTTGTGGGGTGGCGACAGCTTTGCTCCCTCTGGCCTATTATATC	540				
Dd	990	CTGGTAGACACTGGGTTGTGGGGTGGCGACAGCTTTGCTCCCTCTGGCCTATTATATC	931				
Qy	541	CTGGTACTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCCCGGCTTACACCAAC	600				
Dd	930	CTGGTACTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCCCGGCTTACACCAAC	871				
Qy	601	ATCCTCATAGGCAATCTACTTTGCTTGGGCTACGAGTGTGGCACTCTTATTGCTC	660				
Dd	870	ATCCTCATGGGCATCTACTTTGCTTGGGCTACGAGTGTGGCACTCTTATTGCTC	811				
Qy	661	ATCCACCGCAGGTCAAACGACGACACAGCACTGGACCAATAACAAGTTGCGACAGGCA	720				
Dd	810	ATCCACCGCAGGTCAAACGACGACACAGCACTGGACCAATAACAAGTTGCGACAGGCA	751				
Qy	721	AGCATCCAATCCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGTGTTCCAGGAG	780				
Dd	750	AGCATCCAATCCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGTGTTCCAGGAG	691				
Qy	781	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT	840				
Dd	690	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT	631				
Qy	841	GCTGCCACCCACAGACCTTGGAAAGGGACTCATCAGAAGTGGGAGACCCAGATCAACAGC	900				
Dd	630	GCTGCCACCCACAGACCTTGGAAAGGGACTCATCAGAAGTGGGAGACCCAGATCAACAGC	571				
Qy	901	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAACATCTGCCAAGCCAGCCCA	960				
Dd	570	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAACATCTGCCAAGCCAGCCCA	511				
Qy	961	ATTAAGAGGACGACAGAGCTCCCGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	1020				
Dd	510	ATTAAGAGGACGACAGAGCTCCCGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	451				
Qy	1021	TGTTTTGCTGTCTCTGCTTTGCCCTGAGCTACATCCOCTTCTTGTGCTGCTCAACATT	1080				

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Db.      450  TGTTTTGCTGTGTTCTCTGCTTTGGCCGTGAGCTCATCCCTTCTCTGTGCTCACATT 391
Qy      1081  CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTCTGCCAACCTCACTGG 1140
Db      390  CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGTCCAACTCACTGG 331
Qy      1141  CTCGAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAAACGCCAATTCGCCCAAGCA 1200
Db      330  CTCGAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAAACGCCAATTCGCCCAAGCA 271
Qy      1201  TATGGGCTCCATTTTAAAGAGAGGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1260
Db      270  TATGGCTCCATTTTAAAGAGAGGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 211
Qy      1261  CTTAGTACCAGAAATTCAGAGCTGTCTCTCTCCAGACCCAAAAGTGGC 1306
Db      210  CCTAGTCACCAAGATTCCAGACTGTCTCTCCAGGACCAAAGTGGC 165

RESULT 7
US-09-764-893-130
; Sequence 130, Application US/09764893
; Publication No. US20020086330A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: Puz09
; CURRENT APPLICATION NUMBER: US/09/764,893
; PRIOR FILING DATE: 2001-01-19
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-893-130

Query Match          99.6%; Score 1306; DB 13; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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10

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QY 481 CTGCTGAGCAGCTGGTGTGGGGTGGCGAGCTTTGCTCCCTCTGGCGCTATTATATC 540
Db 1057 CTGCTGAGCAGCTGGTGTGGGGTGGCGAGCTTTGCTCCCTCTGGCGCTATTATATC 1116
QY 541 CTGCTGAGCTGAGTCTGACCTGAGCTTTGACCGCATCCGAGCCCGGCTTACACCAAC 600
Db 1117 CTGCTGAGCTGAGTCTGACCTGAGCTTTGACCGCATCCGAGCCCGGCTTACACCAAC 1176
QY 601 ATCTCTATGGGCACTACTTTGCTTGGGCTGAGCAGTGTGGCACTTTCTATTGCTTC 660
Db 1177 ATCTCTATGGGCACTACTTTGCTTGGGCTGAGCAGTGTGGCACTTTCTATTGCTTC 1236
QY 661 ATCCACCGCAGGTCACACGAGCAGCAGGCACTGACCAATACAAAGTTGCGACAGGCA 720
Db 1237 ATCCACCGCAGGTCACACGAGCAGCAGGCACTGACCAATACAAAGTTGCGACAGGCA 1296
QY 721 AGCATCCACTCCAAACCTATGTCGAGGCACTGAGGCCATGCTGCTGCTTCCAGGAG 780
Db 1297 AGCATCCACTCCAAACCTATGTCGAGGCACTGAGGCCATGCTGCTGCTTCCAGGAG 1356
QY 781 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 840
Db 1357 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 1416
QY 841 GCTGCCACCCAGACCCCTGGAAAGGGGACTCATCAGAGTGGGAGACCAAGATCAACAGC 900
Db 1417 GCTGCCACCCAGACCCCTGGAAAGGGGACTCATCAGAGTGGGAGACCAAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGCCAGGCCA 960
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGCCAGGCCA 1536
QY 961 ATTAAGGAGCAGAGAGCTCCGGATTTTCATCGGAATTTGGAGGAGTGAATCGAATG 1020
Db 1537 ATTAAGGAGCAGAGAGCTCCGGATTTTCATCGGAATTTGGAGGAGTGAATCGAATG 1596
QY 1021 TGTTTTGCTGTGTTCTCTGCTTTGCTGCTGAGCTACATCCCTTTCTGCTGCTCAACAT 1080
Db 1597 TGTTTTGCTGTGTTCTCTGCTTTGCTGCTGAGCTACATCCCTTTCTGCTGCTCAACAT 1656
QY 1081 CTGATGTCAGAGTCCAGGCTCCCGGCTGGTCCACATGCTTGTGCCAAGCTCACTGG 1140
Db 1657 CTGATGTCAGAGTCCAGGCTCCCGGCTGGTCCACATGCTTGTGCCAAGCTCACTGG 1716
QY 1141 CTCAATGGTTGCACTCAACCTGCTCTATGAGCCATGAACCGCCAAATTCGCGCAAGCA 1200
Db 1717 CTCAATGGTTGCACTCAACCTGCTCTATGAGCCATGAACCGCCAAATTCGCGCAAGCA 1776
QY 1201 TATGGCTCCATTTAAAGAGGCGCCGAGTTCCATAGGTTCCATAGGTTCCATAGGTTGAC 1260
Db 1777 TATGGCTCCATTTAAAGAGGCGCCGAGTTCCATAGGTTCCATAGGTTCCATAGGTTGAC 1836
QY 1261 CCTAGTCACCAAGATTGAGGACTGCTCTCCAGGACCAAGTGGC 1306
Db 1837 CCTAGTCACCAAGATTGAGGACTGCTCTCCAGGACCAAGTGGC 1882

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RESULT 8
US-10-073-865-130
; Sequence 130, Application US/10073865
; Publication No. US20030044904A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: Puz09C1
; CURRENT APPLICATION NUMBER: US/10/073.865
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 2046

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-073-865-130

Query Match 99.6%; Score 1306; DB 15; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATGCTAGTGTGATTCCTCTCTCCACCTCTGCTCTTTAGCTCTATC 60
Db 577 TTGAATGCTAGTGTGATTCCTCTCTCCACCTCTGCTCTTTAGCTCTATC 636
QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCTGTACCATGAGTCTGTCTGGGTATCGT 120
Db 637 ATGTGGAACAGCTCTGACGCCAACTTCTCTGTACCATGAGTCTGTCTGGGTATCGT 696
QY 121 TATGTTGAGTGTAGTGGGGGTGTGTGCTGTGACAGCAGCGTGGGCAATGTGCTC 180
Db 697 TATGTTGAGTGTAGTGGGGGTGTGTGCTGTGACAGCAGCGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGGCTTTGGCCATCCAGCCCAAGCTCCGTTACCCGATTCAACCTCTCATAGCC 240
Db 757 ACCCTACTGGGCTTTGGCCATCCAGCCCAAGCTCCGTTACCCGATTCAACCTCTCATAGCC 816
QY 241 AACCTCAACACTGGGTGATCTCTCTATGACAGCTCTTTCAGCCCTTCTCTGTGGACAC 300
Db 817 AACCTCAACACTGGGTGATCTCTCTATGACAGCTCTTTCAGCCCTTCTCTGTGGACAC 876
QY 301 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCTCTCTT 360
Db 877 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCTCTCTT 936
QY 361 TTGCTCTCAATTTCTGTCTCATCTGACCTCTGCTCTATCGCACTGGGAGCGTACTCTC 420
Db 937 TTGCTCTCAATTTCTGTCTCATCTGACCTCTGCTCTATCGCACTGGGAGCGTACTCTC 996
QY 421 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGATAGTCTGGCA 480
Db 997 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGATAGTCTGGCA 1056
QY 481 CTGCTGAGCAGCTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 540
Db 1057 CTGCTGAGCAGCTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 1116
QY 541 CTGCTGAGCAGCTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 600
Db 1117 CTGCTGAGCAGCTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 1176
QY 601 ATCTCTATGGGCACTACTTTGCTTGGGCTGAGCAGTGTGGCACTTTCTATTGCTTC 660
Db 1177 ATCTCTATGGGCACTACTTTGCTTGGGCTGAGCAGTGTGGCACTTTCTATTGCTTC 1236
QY 661 ATCCACCGCAGGTCACACGAGCAGCAGGCACTGACCAATACAAAGTTGCGACAGGCA 720
Db 1237 ATCCACCGCAGGTCACACGAGCAGCAGGCACTGACCAATACAAAGTTGCGACAGGCA 1296
QY 721 AGCATCCACTCCAAACCTATGTCGAGGCACTGATGAGGCCATGCTGCTGCTTCCAGGAG 780
Db 1297 AGCATCCACTCCAAACCTATGTCGAGGCACTGATGAGGCCATGCTGCTGCTTCCAGGAG 1356
QY 781 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 840
Db 1357 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 1416
QY 841 GCTGCCACCCAGACCCCTGGAAAGGGGACTCATCAGAGTGGGAGACCAAGATCAACAGC 900
Db 1417 GCTGCCACCCAGACCCCTGGAAAGGGGACTCATCAGAGTGGGAGACCAAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGCCAGGCCA 960
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGCCAGGCCA 1536
QY 961 ATTAAGGAGCAGAGAGCTCCGGATTTTCATCGGAATTTGGAGGAGTGAATCGAATG 1020

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; CURRENT APPLICATION NUMBER: US/09/826,508
 ; CURRENT FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 37
 ; LENGTH: 1498
 ; TYPE: DNA
 ; ORGANISM: HOMO SAPIENS
 US-09-826-508-37

Query Match 95.8%; Score 1256.4; DB 9; Length 1498;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	49	TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG	108
DB	64	TCAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG	123
QY	109	CTGGCTATCGTTATGTTGACGTTAGCTGGGGGTGTTGGTGGTGTGACAGGACCGTG	158
DB	124	CTGGCTATCGTTATGTTGACGTTAGCTGGGGGTGTTGGTGGTGTGACAGGACCGTG	183
QY	169	GGCAATGTGCTCACCTACTGGCTTGGCCATCCAGGCCAGCTCCGTACCCGATTCAAC	228
DB	184	GGCAATGTGCTCACCTACTGGCTTGGCCATCCAGGCCAGCTCCGTACCCGATTCAAC	243
QY	229	CTGCTCATAGCCAACTCAACTGGCTGATCTCTTACTGACGGTCTCTTACGCCCTTC	288
DB	244	CTGCTCATAGCCAACTCAACTGGCTGATCTCTTACTGACGGTCTCTTACGCCCTTC	303
QY	289	TCTGTGACACCTACCTCCACTGCACCTGGGACCGGTGCCACCTTCTCGAGGATTTT	348
DB	304	TCTGTGACACCTACCTCCACTGCACCTGGGACCGGTGCCACCTTCTCGAGGATTTT	363
QY	349	GGGCTCTCTTTTGGCTCCAACTTGTCTCTCACTGCTGACCTCTGCTCTCATCGCACTG	408
DB	364	GGGCTCTCTTTTGGCTCCAACTTGTCTCTCACTGCTGACCTCTGCTCTCATCGCACTG	423
QY	409	GGAGCTACCTCTCATGCCCCACCTTAACTTTTCCCAAGTTTTCAGTGCACGAGGG	468
DB	424	GGAGCTACCTCTCATGCCCCACCTTAACTTTTCCCAAGTTTTCAGTGCACGAGGG	483
QY	469	ATAGTGTGGCACTGGTGGACACCTGGTGTGGGGCTGGCCAGCTTGTCTCCCTCTGG	528
DB	484	ATAGTGTGGCACTGGTGGACACCTGGTGTGGGGCTGGCCAGCTTGTCTCCCTCTGG	543
QY	529	CCTATTATATCTCTGGTACCTGTAGTCTGACCTGTGACCTTTGACCGCATCCGAGCCGG	588
DB	544	CCTATTATATCTCTGGTACCTGTAGTCTGACCTGTGACCTTTGACCGCATCCGAGCCGG	603
QY	589	CCTTTACACCACTCTCATGGGATCTACTTGTGTGGTGTGGCTTCAGCAGTGTGGCATC	648
DB	604	CCTTTACACCACTCTCATGGGATCTACTTGTGTGGTGTGGCTTCAGCAGTGTGGCATC	663
QY	649	TTCTATTGCTCATCCACCGCCAGTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	708
DB	664	TTCTATTGCTCATCCACCGCCAGTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	723
QY	709	TTGGCAGGCAAGCATCCCTCAACCATCTGGCCAGGACTGATGAGGCCATGCTCTGGT	768
DB	724	TTGGCAGGCAAGCATCCCTCAACCATCTGGCCAGGACTGATGAGGCCATGCTCTGGT	783
QY	769	CGTTTCCAGGAGCTGGACAGCAGTGTAGCATCAGGAGGCCACCTGAGGGGATTTTCATCT	828
DB	784	CGTTTCCAGGAGCTGGACAGCAGTGTAGCATCAGGAGGCCACCTGAGGGGATTTTCATCT	843
QY	829	GAGCCAGTCACTGTGTCACACCCAGCCTTGAAGGGGACTCATCAGAGTGGGAGAC	888
DB	844	GAGCCAGTCACTGTGTCACACCCAGCCTTGAAGGGGACTCATCAGAGTGGGAGAC	903
QY	889	CAGATCAACAGCAGAGAGCTTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCC	948
DB	904	CAGATCAACAGCAGAGAGCTTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCC	963

RESULT 11

US-10-225-567A-584
 ; Sequence 584, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lifespan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1930-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 584
 ; LENGTH: 1546
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-225-567A-584

Query Match 95.8%; Score 1256.4; DB 15; Length 1546;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	49	TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG	108
DB	79	TCAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG	138
QY	109	CTGGCTATCGTTATGTTGACGTTAGCTGGGGGTGTTGGTGGTGTGACAGGACCGTG	168
DB	139	CTGGCTATCGTTATGTTGACGTTAGCTGGGGGTGTTGGTGGTGTGACAGGACCGTG	198
QY	169	GGCAATGTGCTCACCTACTGGCTTGGCCATCCAGGCCAGCTCCGTACCCGATTCAAC	228
DB	199	GGCAATGTGCTCACCTACTGGCTTGGCCATCCAGGCCAGCTCCGTACCCGATTCAAC	258
QY	229	CTGCTCATAGCCAACTCAACTGGCTGATCTCTTACTGACGGTCTCTTACGCCCTTC	288
DB	259	CTGCTCATAGCCAACTCAACTGGCTGATCTCTTACTGACGGTCTCTTACGCCCTTC	318
QY	289	TCTGTGGACACCTACCTCCACTGGCGCACCGGTGCGCACCTTCTCGAGGGATTTT	348
DB	319	TCTGTGGACACCTACCTCCACTGGCGCACCGGTGCGCACCTTCTCGAGGGATTTT	378


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349 GGGCTCCTCTCTTTTGGCTCCAAATCTGTCTCCATCTGCTGACCTCTGCTCTCATCGCACTG 408
Db      |||
379 GGGCTCCTCTCTTTTGGCTCCAAATCTGTCTCCATCTGCTGACCTCTGCTCTCATCGCACTG 438
Qy      |||
409 GAGCGTACCTCTCTATGCTCCCACTTAAAGCTTTTCCCAAGTTTTCAGTGCACAGGGG 468
Db      |||
439 GAGCGTACCTCTCTATGCTCCCACTTAAAGCTTTTCCCAAGTTTTCAGTGCACAGGGG 498
Qy      |||
469 ATAGTGTGCACTGCTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528
Db      |||
499 ATAGTGTGCACTGCTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 558
Qy      |||
529 CTTATTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
Db      |||
559 CTTATTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 618
Qy      |||
589 CTTATACCACTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648
Db      |||
619 CTTATACCACTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 678
Qy      |||
649 TTTATTGCTCTATCCACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
Db      |||
679 TTTATTGCTCTATCCACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 738
Qy      |||
709 TTGGGACAGCAAGCATCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
Db      |||
739 TTGGGACAGCAAGCATCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 798
Qy      |||
769 CGTTTCCAGAGCTGAGCAAGCATCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
Db      |||
799 CGTTTCCAGAGCTGAGCAAGCATCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 858
Qy      |||
829 GAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
Db      |||
859 GAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 918
Qy      |||
889 GAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
Db      |||
919 GAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 978
Qy      |||
949 AAAGCCGAGCAATTAAGAGGAGCAGAGAGCTCCGGAATTTCTTTCATCGGAATTTGGGA 1008
Db      |||
979 AAAGCCGAGCAATTAAGAGGAGCAGAGAGCTCCGGAATTTCTTTCATCGGAATTTGGGA 1038
Qy      |||
1009 GTGACTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
Db      |||
1039 GTGACTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098
Qy      |||
1069 CTGCTCAACATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1128
Db      |||
1099 CTGCTCAACATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1158
Qy      |||
1129 AACTCTACCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
Db      |||
1159 AACTCTACCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1218
Qy      |||
1189 TTCCGCCAAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1248
Db      |||
1219 TTCCGCCAAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1278
Qy      |||
1249 TAGAAGTGTGACCTAGTACCAAGATTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1306
Db      |||
1279 TAGAAGTGTGACCTAGTACCAAGATTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1336

```

RESULT 12

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US-09-798-710-1
; Sequence 1, Application US/09798710
; Publication No. US20020187947A1
; GENERAL INFORMATION:
; APPLICANT: Javai, Gabor
; APPLICANT: Cooper, Paul Roy
; APPLICANT: Yousefi, Shida

```

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; TITLE OF INVENTION: No. US20020187947A1e1. Gene
; FILE REFERENCE: 4-31328A/H026
; CURRENT APPLICATION NUMBER: US/09/798,710
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/XXX,XXX
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-09-798-710-1

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Query Match      95.8%; Score 1256.4; DB 9; Length 1595;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      49  TTAGCCTCTATCATGCTGGAACAGCTCTGACGCCAACTTCTCTGCTACATGAGTCTGTG 108
Db      |||
Qy      128 TCAGCCTCTATCATGCTGGAACAGCTCTGACGCCAACTTCTCTGCTACATGAGTCTGTG 187
Db      |||
Qy      109 CTGGGCTATCGTTATGTTGCAAGTTAGCTGGGGGTGGTGGCTGTGACAGGACCCGTG 168
Db      |||
Qy      188 CTGGGCTATCGTTATGTTGCAAGTTAGCTGGGGGTGGTGGCTGTGACAGGACCCGTG 247
Qy      169 GCAATGTGCTCACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 228
Db      |||
Qy      248 GCAATGTGCTCACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 307
Qy      229 CTGCTCATAGCCACCTCACACTGGCTGATCTCTCTACTGACGCTCTCTTTCAGCCCTTC 288
Db      |||
Qy      308 CTGCTCATAGCCACCTCACACTGGCTGATCTCTCTACTGACGCTCTCTTTCAGCCCTTC 367
Qy      289 TCTGTGGACACCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 348
Db      |||
Qy      368 TCTGTGGACACCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 427
Qy      349 GGGCTCCTCTCTTTTGGCTCCAAATCTGTCTCCATCTGCTGACCTCTGCTCTATCGCACTG 408
Db      |||
Qy      428 GGGCTCCTCTCTTTTGGCTCCAAATCTGTCTCCATCTGCTGACCTCTGCTCTATCGCACTG 487
Qy      409 GAGCGTACCTCTCTATGCTCCCACTTAAAGCTTTTCCCAAGTTTTCAGTGCACAGGGG 468
Db      |||
Qy      488 GAGCGTACCTCTCTATGCTCCCACTTAAAGCTTTTCCCAAGTTTTCAGTGCACAGGGG 547
Qy      469 ATAGTGTGCACTGCTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528
Db      |||
Qy      548 ATAGTGTGCACTGCTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 607
Qy      529 CCTATTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
Db      |||
Qy      608 CCTATTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 667
Qy      589 CTTTACACCACTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648
Db      |||
Qy      668 CTTTACACCACTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 727
Qy      649 TTCTATTGCTCTATCCACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
Db      |||
Qy      728 TTCTATTGCTCTATCCACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787
Qy      709 TTGCGACAGGCAAGCATCTCACTCCAAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
Db      |||
Qy      788 TTGCGACAGGCAAGCATCTCACTCCAAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847
Qy      769 CGTTTCCAGAGCTGGAACAGAGGTTAGCATCAGAGGACCCAGTGGAGGATTTTCATCT 828
Db      |||
Qy      848 CGTTTCCAGAGCTGGAACAGAGGTTAGCATCAGAGGACCCAGTGGAGGATTTTCATCT 907
Qy      829 GAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
Db      |||
Qy      908 GAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967

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GENERAL INFORMATION:
 ; APPLICANT: HAGA, TATSUYA
 ; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: 31671-186347
 ; CURRENT APPLICATION NUMBER: US/10/343,650A
 ; CURRENT FILING DATE: 2003-07-21
 ; PRIOR APPLICATION NUMBER: JP 2000/237818
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: JP 2001/34434
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 694
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 45
 ; LENGTH: 1191
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1191)
 US-10-343-650A-45

Query Match 90.6%; Score 1191; DB 13; Length 1191;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	61	ATGTGGAAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGTGGGCTATCGT	120
DB	1	ATGTGGAAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGTGGGCTATCGT	60
QY	121	TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGACACCGTGGGCAATGTGCTC	180
DB	61	TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGACACCGTGGGCAATGTGCTC	120
QY	181	ACCTTACTGCGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGCTCATAGCC	240
DB	121	ACCTTACTGCGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGCTCATAGCC	180
QY	241	AACCTCAGCTGCTGATCTCTACTGACAGCTCTCTCAGCCCTCTCAGCCCTCTCTGTGGACAC	300
DB	181	AACCTCAGCTGCTGATCTCTACTGACAGCTCTCTCAGCCCTCTCTCAGCCCTCTCTGTGGACAC	240
QY	301	TACCTCCACCTGCACTGGCCAGCCGCTGTCACACCTTCTGCAGGGTATTGGGCTCCCTCTT	360
DB	241	TACCTCCACCTGCACTGGCCAGCCGCTGTCACACCTTCTGCAGGGTATTGGGCTCCCTCTT	300
QY	361	TTTGGCTCCAAATCTGTCTCCATCTTCAGCCCTCTGCTATGCTGCTGGAAGCTACCTC	420
DB	301	TTTGGCTCCAAATCTGTCTCCATCTTCAGCCCTCTGCTATGCTGCTGGAAGCTACCTC	360
QY	421	CTCATTTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGGGCA	480
DB	361	CTCATTTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGGGCA	420
QY	481	CTGGTGAGCACTGGTGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG	540
DB	421	CTGGTGAGCACTGGTGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG	480
QY	541	CTGGTGAGCACTGGTGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG	600
DB	481	CTGGTGAGCACTGGTGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG	540
QY	601	ATCCTCATGGGCACTTACTTTGTGCTTGGGCTCAGCAGTGTGGGCACTTCTATTGGCCTC	660
DB	541	ATCCTCATGGGCACTTACTTTGTGCTTGGGCTCAGCAGTGTGGGCACTTCTATTGGCCTC	600
QY	661	ATCCAGCGCCAGCTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	720
DB	601	ATCCAGCGCCAGCTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	660
QY	721	AGCATCCACTCCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTGGTTCAGGAG	780
DB	661	AGCATCCACTCCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTGGTTCAGGAG	720

QY	781	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGAGGATTTTCATCTGAGCCAGTCAGT	840
DB	721	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGAGGATTTTCATCTGAGCCAGTCAGT	780
QY	841	GCTGCCACACCCAGACCCCTGGAGGGGACTCATCAGAAGTGGGAGACAGATCAACAGC	900
DB	781	GCTGCCACACCCAGACCCCTGGAGGGGACTCATCAGAAGTGGGAGACAGATCAACAGC	840
QY	901	AAAGAGAGCTAAGCAGATGCGAGAGAAAGCCCTCCAGAGGATCTGCCAAAGCCCGAGCA	960
DB	841	AAAGAGAGCTAAGCAGATGCGAGAGAAAGCCCTCCAGAGGATCTGCCAAAGCCCGAGCA	900
QY	961	ATTAAGGAGGAGGAGGAGCTCCCGGATTTCTTCATCGGAATTTGGGAAGGTCGATCGAATG	1020
DB	901	ATTAAGGAGGAGGAGGAGCTCCCGGATTTCTTCATCGGAATTTGGGAAGGTCGATCGAATG	960
QY	1021	TGTTTTGCTGTGTTCTCTCTGCTTTCGCTGAGCTACATCCCTCTCTCTGCTGCTCAACAT	1080
DB	961	TGTTTTGCTGTGTTCTCTCTGCTTTCGCTGAGCTACATCCCTCTCTCTGCTGCTCAACAT	1020
QY	1081	CTGGATGCGAGGTCAGGCTCCCGGGTGGTCCACATGCTTGTGTCACCACTCACCTGG	1140
DB	1021	CTGGATGCGAGGTCAGGCTCCCGGGTGGTCCACATGCTTGTGTCACCACTCACCTGG	1080
QY	1141	CTCAATGTTGATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA	1200
DB	1081	CTCAATGTTGATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA	1140
QY	1201	TATGGCTCCATTTTAAAGAGGGGCCCGGAGTTTTCATAGGCTCCATTAG	1251
DB	1141	TATGGCTCCATTTTAAAGAGGGGCCCGGAGTTTTCATAGGCTCCATTAG	1191

RESULT 15

US-10-094-417-3
 ; Sequence 3, Application US/10094417
 ; Publication No. US20030045685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tian, Hui
 ; APPLICANT: Zhao, Jiayang
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: No. US20030045685A1:el Receptors
 ; FILE REFERENCE: 018781-008110US
 ; CURRENT APPLICATION NUMBER: US/10/094,417
 ; CURRENT FILING DATE: 2002-06-10
 ; PRIOR APPLICATION NUMBER: US 09/802,803
 ; PRIOR FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: US 60/276,649
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1188
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1188)
 ; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
 US-10-094-417-3

Query Match 90.6%; Score 1188; DB 15; Length 1188;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 61 ATGTGGAAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGTGGGCTATCGT 120
 DB 1 ATGTGGAAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGTGGGCTATCGT 60

1141 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1188

121 TATGTTGAGTTAGTCTGGGGGTTGGTGGCTGTGACAGGACCGTGGGCAATGTCTC 180
61 TATGTTGAGTTAGTCTGGGGGTTGGTGGCTGTGACAGGACCGTGGGCAATGTCTC 120
181 ACCCTACTGGCTTTGGCCATCCAGCCCAAGTCCTCGTACCCGATTCAACCTGCTCATAGCC 240
121 ACCCTACTGGCTTTGGCCATCCAGCCCAAGTCCTCGTACCCGATTCAACCTGCTCATAGCC 180
241 AACCTCACACTGGCTGTCTCTCTACTGCAAGCTCTCTTCAAGCCCTTCTCTGTGGACAC 300
181 AACCTCACACTGGCTGTCTCTCTACTGCAAGCTCTCTTCAAGCCCTTCTCTGTGGACAC 240
301 TACCTCCACCTGCACTGGCCGACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCTCCCTT 360
241 TACCTCCACCTGCACTGGCCGACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCTCCCTT 300
361 TTTGGCTCCAAATTTGCTCTCATCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC 420
301 TTTGGCTCCAAATTTGCTCTCATCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC 360
421 CTCAATGGCCACCTTACGCTTTTCCCAAGTTTTCAGTGGCCAGGGATAGTCTGGCA 480
361 CTCAATGGCCACCTTACGCTTTTCCCAAGTTTTCAGTGGCCAGGGATAGTCTGGCA 420
481 CTGGTGACACCTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGCGCTATTTATATC 540
421 CTGGTGACACCTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGCGCTATTTATATC 480
541 CTGGTACCTGTAGTCTGCACTGAGCTTTGACCGCATCCGAGCCCGGCTTACACACC 600
481 CTGGTACCTGTAGTCTGCACTGAGCTTTGACCGCATCCGAGCCCGGCTTACACACC 540
601 ATCTCTATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 660
541 ATCTCTATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
661 ATCCACCCGCGAGGTCAACAGCAGCAGCAGCAGCTGGACCAATACAAAGTTGGCAGGCA 720
601 ATCCACCCGCGAGGTCAACAGCAGCAGCAGCAGCTGGACCAATACAAAGTTGGCAGGCA 660
721 AGCATCCACTCAACCATGTGGCCAGCAGCTGATGAGCCATGCTGCTTTCCAGGAG 780
661 AGCATCCACTCAACCATGTGGCCAGCAGCTGATGAGCCATGCTGCTTTCCAGGAG 720
781 CTGACACAGCTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCAGT 840
721 CTGACACAGCTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCAGT 780
841 GCTGCCACCCAGCCAGCTGAGAGGGGACTCATCAGAGTGGGAGACCAAGTCAACAGC 900
781 GCTGCCACCCAGCCAGCTGAGAGGGGACTCATCAGAGTGGGAGACCAAGTCAACAGC 840
901 AAGGAGCTTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCGAGCCA 960
841 AAGGAGCTTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCGAGCCA 900
961 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
901 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
1021 TGTTTTGCTGTCTCTCTGCTTTGCTGCTGAGCTACATCCCTTCTTGTCTCAACATT 1080
961 TGTTTTGCTGTCTCTCTGCTTTGCTGCTGAGCTACATCCCTTCTTGTCTCAACATT 1020
1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCAACCTCACCTGG 1140
1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCAACCTCACCTGG 1080
1141 CTCAATGTTGCATCAACCTGCTGTCTATGCGCCATGACCCCAATTCGCGCAAGCA 1200
1081 CTCAATGTTGCATCAACCTGCTGTCTATGCGCCATGACCCCAATTCGCGCAAGCA 1140
1201 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1248

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:14:09 ; Search time 3805.67 Seconds
(without alignments)
10287.096 Million cell updates/sec

Title: US-10-029-436-1

Perfect score: 1311

Sequence: 1 ttgaatgctaggtcttgatt.....caggaccacaaaggcaggtta 1311

Scoring table: IDENTITY NUC

Capop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estind:*

4: em_estmd:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_ptg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1191	90.8	1191	29	AY404787 Homo sapi
2	1116.2	85.1	1187	29	AY404788 Pan trogl
3	889.2	67.8	1191	29	AY404789 Mus muscu
4	798.6	60.9	997	13	BX348812 BX348812

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C 5	597	45.5	809	14	CD367121	UI-H-FT2-
C 6	587	44.8	903	13	EX330186	EX330186
C 7	536	40.9	721	14	CD365430	UI-H-FT2-
C 8	525	40.0	736	14	CD366881	UI-H-FT2-
C 9	491	37.5	700	14	CD385279	UI-H-FT2-
C 10	475	36.2	660	12	EM782245	UI-E-E70-
C 11	464	35.4	1201	13	EX336527	EX336527
C 12	448.4	34.2	496	13	EX097926	EX097926
C 13	445.6	34.0	621	14	CD470995	Leuko85_3
C 14	442	33.7	650	14	CD366344	UI-H-FT1-
C 15	426.6	32.5	660	10	BF667988	60212233
C 16	419	32.0	542	12	BM254098	BM254098
C 17	415.4	31.7	829	10	BE982111	601644675
C 18	412.8	31.5	553	12	BM258181	522891 MA
C 19	409	31.2	588	12	BM680856	UI-E-E70-
C 20	399.8	30.5	726	14	CF739045	UI-M-HD0-
C 21	392.6	29.9	532	14	CD536450	LeukoN6_7
C 22	392	29.9	499	12	BI773943	465705 MA
C 23	391.4	29.9	498	14	CB221964	11L22B6_B
C 24	386	29.4	474	12	BM105642	509140 MA
C 25	368.8	28.1	533	10	BE502961	h281902.x
C 26	367	28.0	526	12	BG232061	BG232061
C 27	361.6	27.6	807	10	BF167811	601774636
C 28	360	27.5	635	14	CD470023	Leuko84_1
C 29	354	27.0	518	9	AI392922	tg10g11.x
C 30	353.2	26.9	458	14	CD464412	Leuko84_3
C 31	352	26.8	475	10	BF654980	275349 MA
C 32	342.4	26.1	572	13	EX511990	EX511990
C 33	342.2	26.1	588	14	CD465714	LeukoN1_7
C 34	340.4	26.0	585	14	CD464304	LeukoN4_3
C 35	339.2	25.9	588	14	CD470028	Leuko84_1
C 36	338.8	25.8	572	14	CD470901	Leuko85_3
C 37	337.2	25.7	584	14	CD536362	LeukoN6_7
C 38	332.2	25.3	587	14	CD464888	LeukoN4_5
C 39	323.6	24.7	551	14	CD464476	LeukoN4_4
C 40	311.4	23.8	528	12	BG235994	na20f04
C 41	299.2	22.8	368	10	BF706009	280136 MA
C 42	288.2	22.0	497	10	AW213499	ums56b11.y
C 43	277	21.1	441	10	BE467421	h265f10.x
C 44	276	21.1	444	10	BF111095	7n43d11.x
C 45	275.4	21.0	441	10	BE550808	7D59C04.x

ALIGNMENTS

RESULT 1	AY404787	1191 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	Homo sapiens GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	Genomic survey sequence.				
ACCESSION	AY404787				
VERSION	AY404787.1	GI:39760764			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Clark,A.G., Glatowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1191)				
AUTHORS	Clark,A.G., Glatowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1..1191
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1191
/gene="GPR84"
/locus_tag="HCM2007"
ORIGIN
Query Match 90.8%; Score 1191; DB 29; Length 1191;
Best Local Similarity 100.0%; Pred. No. 7e-291;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 ATGTGGAAACAGCTCTGACGCCCAACTTCTCTGCTACCATGAGTCTGTGGGCTATCGT 120
Db 1 ATGTGGAAACAGCTCTGACGCCCAACTTCTCTGCTACCATGAGTCTGTGGGCTATCGT 60
QY 121 TATGTTGAGTAGTCTGGGGGGTGGTGGTGGTGTGACGACACCGTGGGCAATGTGCTC 180
Db 61 TATGTTGAGTAGTCTGGGGGGTGGTGGTGGTGTGACGACACCGTGGGCAATGTGCTC 120
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGTCCGTACCCGATTCAACCTGCTCATAGCC 180
QY 241 AACCTCACACAGTGTGATCTCTCTACTGACAGCTCTTTCAGCCCTTCTCTGTGGACACC 300
Db 181 AACCTCACACAGTGTGATCTCTCTACTGACAGCTCTTTCAGCCCTTCTCTGTGGACACC 240
QY 301 TACCTCCACCTGCATGGCGACCGGTGCCACACCTTCTGCAAGGATTTGGGCTCTCTCTT 360
Db 241 TACCTCCACCTGCATGGCGACCGGTGCCACACCTTCTGCAAGGATTTGGGCTCTCTCTT 300
QY 361 TTGGCTCCATTTCTGCTCATCTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 301 TTGGCTCCATTTCTGCTCATCTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 421 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGGATAGTGTGCA 480
Db 361 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGGATAGTGTGCA 420
QY 481 CTGGTGACACCTGGTGTGGGGGTGGCGAGCTTTGCTCCCTCTGGCCTATTATATC 540
Db 421 CTGGTGACACCTGGTGTGGGGGTGGCGAGCTTTGCTCCCTCTGGCCTATTATATC 480
QY 541 CTGGTACCTGTAGTCTGACCTGAGCTTTGACCGCATCGAGCCGGCTTACACCACC 600
Db 481 CTGGTACCTGTAGTCTGACCTGAGCTTTGACCGCATCGAGCCGGCTTACACCACC 540
QY 601 ATCTCTATGGGCATCTACTTTGCTTGGGCTGAGCAGTGTGCACTTCTTATGTGCTC 660
Db 541 ATCTCTATGGGCATCTACTTTGCTTGGGCTGAGCAGTGTGCACTTCTTATGTGCTC 600
QY 661 ATCCACCGCCAGGTCAACAGCAGCAGCAGCAGCTGACCAATCAAGTTGGCAGCAGCA 720
Db 601 ATCCACCGCCAGGTCAACAGCAGCAGCAGCAGCTGACCAATCAAGTTGGCAGCAGCA 660
QY 721 AGCATCCACTCAACCACTGTGGCCAGCAGTGTATGAGCCCATGCTGTGCTTCCAGGAG 780
Db 661 AGCATCCACTCAACCACTGTGGCCAGCAGTGTATGAGCCCATGCTGTGCTTCCAGGAG 720
QY 781 CTGGACACAGGTAGCATCAGGAGGACCCAGTGCAGGGATTTTCATCTGAGCCAGTCAGT 840
Db 721 CTGGACACAGGTAGCATCAGGAGGACCCAGTGCAGGGATTTTCATCTGAGCCAGTCAGT 780
QY 841 GCTGCCACACCCAGCCCTGGAGGGGACTCATCAGAAAGTGGGAGACCCAGATCAACAGC 900
Db 781 GCTGCCACACCCAGCCCTGGAGGGGACTCATCAGAAAGTGGGAGACCCAGATCAACAGC 840

QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 960
Db 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
QY 961 ATTAAGAGGAGCAGAGAGCTCCGATTTCTCATCGGAATTTGGAGAGTCACTCGAATG 1020
Db 901 ATTAAGAGGAGCAGAGAGCTCCGATTTCTCATCGGAATTTGGAGAGTCACTCGAATG 960
QY 1021 TGTGTTGCTGTGTTCTCTGCTTTGCTGAGTACATCCCTCTTCTGCTGCTCAACATT 1080
Db 961 TGTGTTGCTGTGTTCTCTGCTTTGCTGAGTACATCCCTCTTCTGCTGCTCAACATT 1020
QY 1081 CTGGATGACAGAGTCCAGGCTCCCGGGTGGTGCATGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1021 CTGGATGACAGAGTCCAGGCTCCCGGGTGGTGCATGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1141 CTCATGTTGTCATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGGCCAGCA 1200
Db 1081 CTCATGTTGTCATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGGCCAGCA 1140
QY 1201 TATGCTCCATTTTAAAAAGAGGGCCCGAGTTTCCATAGGCTCCATTAG 1251
Db 1141 TATGCTCCATTTTAAAAAGAGGGCCCGAGTTTCCATAGGCTCCATTAG 1191
RESULT 2
AY404788 1197 bp DNA linear GSS 16-DEC-2003
LOCUS Pan troglodytes GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY404788
VERSION AY404788.1 GI:39760765
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1187)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1187)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,I.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source 1..1187
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1187
/gene="GPR84"
/locus_tag="HCM2007"
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Query Match 85.1%; Score 1116.2; DB 29; Length 1187;
Best Local Similarity 94.4%; Pred. No. 6.7e-272;
Matches 1121; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 61 ATGTGGAAACAGCTCTGACGCCCAACTTCTCTGCTACCATGAGTCTGTGGCTATCGT 120

Db 1 ATGTGGNAACAGCTCTGACGCCAACTTCTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT 60
Qy 121 TATGTTGCACTTATGCTGGGGGGTGGTGGTGGCTGTGTGACAGGCAACCGTGGGCAATGTCCTC 180
Db 61 TATGTTGCACTTATGCTGGGGGGTGGTGGTGGCTGTGTGACAGGCAACCGTGGGCAATGTCCTC 120
Qy 181 ACCTTACTGCTTGGCCATCCAGGCCCAAGCTCCGTACCGGATTCAACCTGCTCATAGCC 240
Db 121 ACCTTACTGCTTGGCCATCCAGGCCCAAGCTCCGTACCGGATTCAACCTGCTCATAGCC 180
Qy 241 AACCTCACACTGGCTGATCTCTCTACTGACAGCTCTCTTACGCCCTTCTCTGTGGACAC 300
Db 181 AACCTCACACTGGCTGATCTCTCTACTGACAGCTCTCTTACGCCCTTCTCTGTGGACAC 240
Qy 301 TACTTCCACTGCACTGGGCGACGGTGGCCACCTTCTGACAGGTAATTTGGGCTCTCTCTT 360
Db 241 TACTTCCACTGCACTGGGCGACGGTGGCCACCTTCTGACAGGTAATTTGGGCTCTCTCTT 300
Qy 361 TTTGGCTTCCAAATCTGTCTCCATCTCCAGCCCTCTGCTCATCGCACTGGGAGCTACCTC 420
Db 301 TTTGGCTTCCAAATCTGTCTCCATCTCCAGCCCTCTGCTCATCGCACTGGGAGCTACCTC 360
Qy 421 CTCAATGGCCACCTTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGGGATAGTCTGGCA 480
Db 361 CTCAATGGCCACCTTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGGGATAGTCTGGCA 420
Qy 481 CTGCTGAGCACTGGGTTGGCGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 540
Db 421 CTGCTGAGCACTGGGTTGGCGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 480
Qy 541 CTGCTGAGCACTGGGTTGGCGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 600
Db 481 CTGCTGAGCACTGGGTTGGCGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 540
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Db 541 ATCTCATGGGCTTACTTTGCTTGGCCTGAGGCTGAGGCTGCTGCTTCTTATTCCTC 600
Qy 661 ATCCACCGCAGCTCAAAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 720
Db 601 ATCCACCGCAGCTCAAAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 660
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Db 661 AGCATCCACTCAACCATGTCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 720
Qy 781 CTGACAGCAGCTAGCTAGCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 840
Db 721 NTGACAGCAGCTAGCTAGCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
Qy 841 GCTGCCACCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 900
Db 781 NNNNNNACCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 840
Qy 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 960
Db 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 900
Qy 961 ATTAAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1020
Db 901 ATTAAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 960
Qy 1021 TGTTTTCTGCTGCTTCTGCTTGGCTGAGCTAGATCCCTCTGCTGCTGCTGCTGCTGCTG 1080
Db 961 TGTTTTCTGCTGCTTCTGCTTGGCTGAGCTAGATCCCTCTGCTGCTGCTGCTGCTGCTG 1020
Qy 1081 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCAGATGCTTGTGCTGCCAAGCTCACTGG 1140
Db 1021 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCAGATGCTTGTGCTGCCAAGCTCACTGG 1080
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Db 1081 CTCAACGGTGGATCAACCTGCTGCTATGAGGCAATGAACCGCAATTCGCGCAAGCA 1140

Qy 1201 TATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCCATAGGCTCCA 1247
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RESULT 3
AY404789 1191 bp DNA linear GSS 16-DEC-2003
LOCUS Mus musculus GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY404789
VERSION AY404789.1 GI:39760766
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1191)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1191)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..1191
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene <1..>1191
/gene="GPR84"
/locus_tag="HCM2007"

ORIGIN
Query Match 67.8%; Score 889.2; DB 29; Length 1191;
Best Local Similarity 84.2%; Pred. No. 2.8e-214;
Matches 1002; Conservative 0; Mismatches 188; Indels 0; Gaps 0;
Qy 61 ATGTGAAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGTGGGCTATCGA 120
Db 1 ATGTGAAACAGCTCAGATGCCAACTTCTCTGCTACCATGAGTCTGTGTGGGCTATCGA 60
Qy 121 TATGTTGCACTTATGCTGGGGGGTGGTGGTGGCTGTGTGACAGGCAACCGTGGGCAATGTCCTC 180
Db 61 TACTTTGCACTTATCTGGGGGGTGGTGGTGGCTGTGTGACAGGCAACCGTGGGCAATGTCCTC 120
Qy 181 ACCCTTACTGGCTTGGCCATCCAGGCCCAAGCTCCGTACCGGATTCAACCTGCTCATAGCC 240
Db 121 ACTCTGCTGGCTTGGCCATCCGTCCCAAGCTCCGAAACCCGCTTCAACCTGCTCATAGCC 180
Qy 241 AACCTCACACTGGCTGATCTCTCTACTGACAGCTCTCTTACGCCCTTCTCTGTGGACAC 300
Db 181 AACCTCACCTGGCTGATCTCTCTACTGACAGCTCTCTTACGCCCTTCTCTGTGGACACA 240
Qy 301 TACTTCCACTGCACTGGGCGACGGTGGCCACCTTCTGACAGGTAATTTGGGCTCTCTCTT 360
Db 241 TACTTCCACTCCATTTGGGTACCGGCGGGTCTCTGTAGAAATTTTGGACTCTCTCTC 300
Qy 361 TTTGGCTTCCAAATCTGTCTCCATCTCCAGCCCTCTGCTCATCGCACTGGGAGCTACCTC 420

Db 301 TTACTTCCAAATTCGTCTCCATCCTCACCCTCTGTCTCATTTGCTAGGACGTACCTC 360
 Qy 421 CTCATTTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGATAGTGTGGCA 480
 Db 361 CTCATTTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGATAGTGTGGCA 420
 Qy 481 CTGTTGACACCTGGTGTGGGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCG 540
 Db 421 CTGTTGACACCTGGTGTGGGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCG 480
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 Db 481 TTGTTGCCAGTGTCTGCACCTGCGAGCTTTGACCGCATCCGAGCCGGCTTACACCA 540
 Qy 601 ATCTCATGGGCATCTACTTTGCTTGGGCTGACGAGTGTGGCATCTTCTTATTCCTC 660
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 Db 661 AGCATTCACCTCAACATGTGGCAGGATGATGAGGCTATGCTGTGCTTCCAGGAG 720
 Qy 781 CTGGACACGAGTTAGCATCAGGAGGACCCAGTCCAGGAGTTTCTATCTGAGCCAGTCA 840
 Db 721 CTGGACACGAGTTAGCATCAGGAGGACCCAGTCCAGGAGTTTCTATCTGAGCCAGT 780
 Qy 841 GCTGCCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 900
 Db 781 GCTGCCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 840
 Qy 901 AAGAGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAG 960
 Db 841 AAGAGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAG 900
 Qy 961 ATTAAGAGGACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAG 1020
 Db 901 ACTGACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAG 960
 Qy 1021 TGTTTGTGTTCTTCTGCTTGGCTGAGTACATCCCTTCTTGTGCTCAACATT 1080
 Db 961 TGCTTGCAGTGTCTTCTGCTTGGCTGAGTACATCCCTTCTTGTGCTCAACATT 1020
 Qy 1081 CTGGATGACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 1140
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 Qy 1141 CTCATGTTGCTATCAACCTTGTGCTTATGACGATGATGACGATGATGACGATGATGAC 1200
 Db 1081 CTCATGTTGCTATCAACCTTGTGCTTATGACGATGATGACGATGATGACGATGATGAC 1140
 Qy 1201 TATGCTCCATTTTAAAGAGGCGCGGAGTTTCCATAGGCTCCATT 1250
 Db 1141 TATGCTCCATTTTAAAGAGGCGCGGAGTTTCCATAGGCTCCATT 1190

RESULT 4
 BX348812
 LOCUS
 DEFINITION BX348812 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1029YE18 5-PRIME, mRNA sequence.
 ACCESSION BX348812
 VERSION BX348812.1 GI:30379347
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 997)
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6847.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0BAG0282C10_CS02667_1&cluster=6847.r.
 Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0BAG0282C10_CS02667_1.
 Location/Qualifiers
 1..997
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1029YE18"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="List strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 60.9%; Score 798.6; DB 13; Length 997;
 Best Local Similarity 98.7%; Pred. No. 2.5e-191;
 Matches 823; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
 QY 252 GCGTATCTCTCTACTGACGCTCTTTCAGCCCTCTCTCTGACACCTACCTCCACCT 311
 Db 15 GCGTATCTCTCTACTGACGCTCTTTCAGCCCTCTCTCTGACACCTACCTCCACCT 74
 QY 312 GCACTGGGGCACCCTGCGACCTTCTGAGGGTATTTGGGCTCTCTCTTTTGGCTCAA 371
 Db 75 GCACTGGGGCACCCTGCGACCTTCTGAGGGTATTTGGGCTCTCTCTTTTGGCTCAA 134
 QY 372 TTCTGTCTCCATCTCTGACCTCTGCTCTCATCGCACTGGGAGCTACCTCTCTATGGCCA 431
 Db 135 TTCTGTCTCCATCTCTGACCTCTGCTCTCATCGCACTGGGAGCTACCTCTCTATGGCCA 194
 QY 432 CCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGATAGTGTGGGACCTGGTGAGCAC 491
 Db 195 CCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGATAGTGTGGGACCTGGTGAGCAC 254
 QY 492 CTGGGTTGTGGCGTGGCGAGCTTTGCTCCCTCTGCGCTATTTATATCTCTGGTACCTGT 551
 Db 255 CTGGGTTGTGGCGTGGCGAGCTTTGCTCCCTCTGCGCTATTTATATCTCTGGTACCTGT 314
 QY 552 AGTCTGACCTGACGCTTTGACCGCATCCGAGGCGGCTTTACACCACTCTCTCATGGG 611
 Db 315 AGTCTGACCTGACGCTTTGACCGCATCCGAGGCGGCTTTACACCACTCTCTCATGGG 374
 QY 612 CATCTACTTTGTGCTTGGGCTCAGCAGTGTGGGATCTTCTATTGCTTCATCCACCGCCA 671
 Db 375 CATCTACTTTGTGCTTGGGCTCAGCAGTGTGGGATCTTCTATTGCTTCATCCACCGCCA 434
 QY 672 GGTCAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 731
 Db 435 GGTCAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 494
 QY 732 GAACTATGTGGCAGGACTGATGAGCCATGCTGCTGCTTTCAGGAGCTGGACAGCAG 791
 Db 495 CAACCATGTGGCAGGACTGATGAGCCATGCTGCTGCTTTCAGGAGCTGGACAGCAG 554
 QY 792 GTTAGCATCAGGAGGACCCAGTGGGGGATTTCTATCTGAGCCAGTCAAGTGTGCCACCA 851
 Db 555 GTTAGCATCAGGAGGACCCAGTGGGGGATTTCTATCTGAGCCAGTCAAGTGTGCCACCA 614
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/db_xref="taxon:9606"
/clone="CS0D1029YE18"
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/primer="Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 44.8%; Score 587; DB 13; Length 903;
Best Local Similarity 98.0%; Pred. No. 1.2e-137;
Matches 593; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 702 ATCAAGTTGGACGAGCAGATCCATCCACCATGTGGCCAGGACTGATGAGCCAT 761
Db |||||
QY 757 ATCCAGGTTGGCAGGCAAGCATCCACTCAACCATGTGCCAGGGCACTAATGAGCCAA 698
Db |||||
QY 762 GCCTGGTCTGTTCCAGAGCTGGACAGCAGGTAGCATCAGGAGGCCAGTCCAGGGAT 821
Db |||||
QY 697 GCCTGGTCTGTTCCAGAGCTGGACAGCAGGTAGCATCAGGAGGCCAGTCCAGGGAT 638
Db |||||
QY 822 TTCATCTGAGCAGTCTGAGTCCACCACCCAGACCCCTGGAGGGGACTCATCAAGAT 881
Db |||||
QY 637 TTCATNTGAGCCAGTCACTGTCGCCACCCAGACCCCTGGAGGGGACTCATCAAGAT 578
Db |||||
QY 882 GGGAGACCATCAACAGCAGAGATGACATGGCAGAGAAAGCCCTCCAGAGC 941
Db |||||
QY 577 GGGAGACCATCAACAGCAGAGATGACATGGCAGAGAAAGCCCTCCAGAGC 518
Db |||||
QY 942 ATCTGCCAAAGCCAGACCAATTAAGAGGAGCAGAGAGCTCCGAGTCTTTCATCGAAT 1001
Db |||||
QY 517 ATCTGCCAAAGCCAGACCAATTAAGAGGAGCAGAGAGCTCCGAGTCTTTCATCGAAT 458
Db |||||
QY 1002 TGGGAAGTGACTCGAATGTTTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1061
Db |||||
QY 457 TGGGAAGTGACTCGAATGTTTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 398
Db |||||
QY 1062 CTCTCTGTCTCAACATTCCTGATGCGAGTCCAGCTCCCGGGTGTGCCATGCT 1121
Db |||||
QY 397 CTCTCTGTCTCAACATTCCTGATGCGAGTCCAGCTCCCGGGTGTGCCATGCT 338
Db |||||
QY 1122 TGCTGCCAACCTCACTCTGGTCAATGTGTGATCAACCTGTCTCTATGAGCCATGAA 1181
Db |||||
QY 337 TGCTGCCAACCTCACTCTGGTCAATGTGTGATCAACCTGTCTCTATGAGCCATGAA 278
Db |||||
QY 1182 CCGCCAAATTCGCGAAGCATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAG 1241
Db |||||
QY 277 CCGCCAAATTCGCGAAGCATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAG 218
Db |||||
QY 1242 GCTCCATTAGAACTGTGACCTAGTACCAGAAATTCAGGACTGTCTCTCCAGGACCAA 1301
Db |||||
QY 217 GCTCCATTAGAACTGTGACCTAGTACCAGAAATTCAGGACTGTCTCTCCAGGACCAA 158
Db |||||
QY 1302 GTGGC 1306
Db |||||
QY 157 GTGGC 153
Db |||||

RESULT 7
CD365430/c
LOCUS
DEFINITION
UI-H-FT2-bjj-1-21-0-UI-s1 NCI-CGAP_F12 Homo sapiens cDNA clone
UI-H-FT2-bjj-1-21-0-UI 3', mRNA sequence.
ACCESSION
CD365430
VERSION
CD365430.1 GI:31149520
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 721)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

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TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLVA=Yes.

FEATURES
Location/Qualifiers
1..721
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/db_xref="taxon:9606"
/clone="UI-H-FT2-bjj-1-21-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP_F12"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP F12 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG TISSUE=Human Lung Aveolar Macrophage TAG_LIB=UI-H-FT2 TAG_SEQ=GGCCATGCGG"

ORIGIN
Query Match 40.9%; Score 536; DB 14; Length 721;
Best Local Similarity 99.8%; Pred. No. 9.2e-125;
Matches 547; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 759 CATGCTCTGTCTTCCAGGAGCTGGACAGCAGCTTAGCATCAGAGGACCCAGTAGGG 818
Db |||||
QY 721 CATGCTCTGTCTTCCAGGAGCTGGACAGCAGCTTAGCATCAGAGGACCCAGTAGGG 662
Db |||||
QY 819 GATTTTCATCTGAGCAGTCACTGTGTCACCACTGAGCCCTGGAGGGGACTCATAGA 878
Db |||||
QY 661 GATTTTCATCTGAGCAGTCACTGTGTCACCACTGAGCCCTGGAGGACTCATAGA 603
Db |||||
QY 879 AGTGGGACCCAGATCAACAGCAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGA 938
Db |||||
QY 602 AGTGGGACCCAGATCAACAGCAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGA 543
Db |||||
QY 939 AGCATCTGCCAAAGCCAGCCAAATTAAGGAGCCAGAGAGCTCCGATTTTTCATCGGA 998
Db |||||
QY 542 AGCATCTGCCAAAGCCAGCCAAATTAAGGAGCCAGAGAGCTCCGATTTTTCATCGGA 483
Db |||||
QY 999 ATTTGGGAGGTGACTCGAATGTTTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1058
Db |||||
QY 482 ATTTGGGAGGTGACTCGAATGTTTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 423
Db |||||
QY 1059 CCCCTTCTTGTCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACAT 1118
Db |||||
QY 422 CCCCTTCTTGTCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACAT 363
Db |||||
QY 1119 GCTTCTGCCAACCTCACTGCTCAATGTTGATCATCAACCTGTGCTCTATGAGCCAT 1178
Db |||||
QY 362 GCTTCTGCCAACCTCACTGCTCAATGTTGATCATCAACCTGTGCTCTATGAGCCAT 303
Db |||||
QY 1179 GAACCGCCAAATTCGCGAAGCATATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCA 1238
Db |||||
QY 302 GAACCGCCAAATTCGCGAAGCATATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCA 243
Db |||||
QY 1239 TAGGCTCCATAGAACTGTGACCTAGTACACAGATTCAGGACTGTCTCTCCAGGACC 1298
Db |||||

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Db      242 TAGGCTCCATTAGACTGTGACCTAGTCACAGAAATTCAGGACTGTCTCCTCCAGACC 183
QY      1299 AAAGTGGC 1306
Db      182 AAAGTGGC 175

RESULT 8
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LOCUS      UI-H-FT2-bj2-k-21-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
DEFINITION      UI-H-FT2-bj2-k-21-0-UI 3', mRNA sequence.
ACCESSION      CD366881
VERSION      1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE      1 (bases 1 to 736)
JOURNAL      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
      Tumor Gene Index
      Unpublished (1997)
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs@mail.nih.gov
      Tissue Procurement: Dr. Gary W. Hunninghake, U of I
      cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
      cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
      DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
      Clone Distribution: Distribution information can be found at
      http://genome.uiowa.edu/distribution/cgap.html
      Seq primer: M13 FORWARD
      POLVA=Yes.

FEATURES
      source
      1..736
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="UI-H-FT2-bj2-k-21-0-UI"
      /issue_type="Aveolar Macrophage"
      /dev_stage="Adult"
      /lab_host="DH10B (Life Technologies)"
      /clone_lib="NCI_CGAP_FT2"
      /notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
      modified polylinker; Site 1: EcoR I; Site 2: Not I;
      NCI CGAP FT2 is a substracted cDNA library constructed from
      a pool of 81 RNA samples from Alveolar Macrophages
      challenged with different treatments. The library was
      substracted according to Bonaldo, Lennon and Soares, Genome
      Research, 6:791-806, 1996. The tissue was provided by Dr.
      Gary W. Hunninghake of the University of Iowa.
      TAG TISSUE=Human Lung Aveolar Macrophage
      TAG LIB=UI-H-FT2
      TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match      40.0%; Score 525; DB 14; Length 736;
Best Local Similarity 99.3%; Pred. No. 5.8e-122;
Matches 558; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY      745 AGGACTGATGAGCCATGCTGCTGTTCCAGAGCTGGACAGAGGTAGCATCAGGA 804
Db      736 AGGACTGATGAGCCATGCTGCTGTTCCAGAGCTGGACAGAGGTAGCATCAGGA 677
QY      805 GGACCCAGTGGGGATTTTCATCTGACCCAGTCAGTGTGCTGCCACCCAGACCCCTGGAA 864
Db      676 GGACCCAGTGA-GGGATTTTCATCTGAGCCAGTCAGTGTGCTGCCACCCAGACCCCTGGAA 618
QY      865 GGGACTCATCAGAGTGGAGACCCAGATCAACAGCAGAGAGCTAAGCAGATGGCAGAG 924
Db      617 -GGGACTCATCAGAGT-GGAGACCCAGATCAACAGCAGAGAGCTAAGCAGATGGCAGAG 560

QY      925 AAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCAAATTAAGGAGCCAGAGCTCCG 984
Db      559 AAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCAAATTAAGGAGCCAGAGCTCCG 500
QY      985 GATTCTTCATCGGAATTTGGGAAGTGACTCGAATGTGTTTGTCTGCTCTCTGCTTT 1044
Db      499 GATTCTTCATCGGAATTTGGGAAGTGACTCGAATGTGTTTGTCTGCTCTCTGCTTT 440
QY      1045 GCCCTGAGCTACATCCCTCTTCTGCTCTCAACATTCGGATGCCAGAGTCCAGGCTCCC 1104
Db      439 GCCCTGAGCTACATCCCTCTTCTGCTCTCAACATTCGGATGCCAGAGTCCAGGCTCCC 380
QY      1105 CGGGTGTTCACATGTTGTCGCAACCTCACCTGGCTCAATGTTGCATCAACCCCTGTG 1164
Db      379 CGGGTGTTCACATGTTGTCGCAACCTCACCTGGCTCAATGTTGCATCAACCCCTGTG 320
QY      1165 CTCATGAGCAGCATGAACCCGCAATTCGGCAAGCATATGGCTCCATTTTAAAGAGGG 1224
Db      319 CTCATGAGCAGCATGAACCCGCAATTCGGCAAGCATATGGCTCCATTTTAAAGAGGG 260
QY      1225 CCCCGAGTTTCCATAGCTCCATTAGAACTGTGACCTAGTCACCCAGATTCAGGACTG 1284
Db      259 CCCCGAGTTTCCATAGCTCCATTAGAACTGTGACCTAGTCACCCAGATTCAGGACTG 200
QY      1285 TCTCTCTCAGGACCAAAAGTGGC 1306
Db      199 TCTCTCTCAGGACCAAAAGTGGC 178

RESULT 9
CD365279/c      700 bp mRNA linear EST 29-MAY-2003
LOCUS      UI-H-FT2-bj2-k-21-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
DEFINITION      UI-H-FT2-bj2-k-21-0-UI 3', mRNA sequence.
ACCESSION      CD365279
VERSION      1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE      1 (bases 1 to 700)
JOURNAL      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
      Tumor Gene Index
      Unpublished (1997)
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs@mail.nih.gov
      Tissue Procurement: Dr. Gary W. Hunninghake, U of I
      cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
      cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
      DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
      Clone Distribution: Distribution information can be found at
      http://genome.uiowa.edu/distribution/cgap.html
      Seq primer: M13 FORWARD
      POLVA=Yes.

FEATURES
      Location/Qualifiers
      1..700
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="UI-H-FT2-bj2-k-21-0-UI"
      /issue_type="Aveolar Macrophage"
      /dev_stage="Adult"
      /lab_host="DH10B (Life Technologies)"
      /clone_lib="NCI_CGAP_FT2"
      /notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
      modified polylinker; Site 1: EcoR I; Site 2: Not I;
      NCI CGAP FT2 is a substracted cDNA library constructed from
      a pool of 81 RNA samples from Alveolar Macrophages
      challenged with different treatments. The library was
      substracted according to Bonaldo, Lennon and Soares, Genome
      Research, 6:791-806, 1996. The tissue was provided by Dr.
      Gary W. Hunninghake of the University of Iowa.
      TAG TISSUE=Human Lung Aveolar Macrophage
      TAG LIB=UI-H-FT2
      TAG_SEQ=GGCCATGCCG"

```

Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Ateolar Macrophage
TAG LIB=UI-H-FT2
TAG_SEQ=GGCCATGCGG

ORIGIN

```

Query Match      37.5%; Score 491; DB 14; Length 700;
Best Local Similarity 99.1%; Pred. No. 2.4e-113; Indels 3; Gaps 3;
Matches 524; Conservative 0; Mismatches 2;

QY 778 GAGCTGGACAGCAGGTTAGCATCAGGAGGAGCCAGTGGGGGATTTTCATCTGAGCCAGTC 837
DB 700 GAGCTGGACAGCAGGTTAGCATCAGGAGGAGCCAGTGGGGGGA-NTCATCTGAGCCAGTC 642

QY 838 AGTCTGCCACCCAGACCCCTGGAGGGGAGTCTATCAGAAGTGGAGACCATCAAC 897
DB 641 AGT-CTGCCACCCAGACCCCTGGGA-GGGACTCATCAGAAGTGGAGACCATCAAC 584

QY 898 ACCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAG 957
DB 583 AGCAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAG 524

QY 958 CCAATTAAGAGAGCCAGAGAGCTCCGGATTTTCATCGGAATTTGGGAAGTGTACTCGA 1017
DB 523 CCAATTAAGAGAGCCAGAGAGCTCCGGATTTTCATCGGAATTTGGGAAGTGTACTCGA 464

QY 1018 ATGTTTGTGTTGTTTCTCTGTTTCCCTGAGTACATCCCTTCTTGTGCTCAAC 1077
DB 463 ATGTTTGTGTTTCTCTGTTTCCCTGAGTACATCCCTTCTTGTGCTCAAC 404

QY 1078 ATTCGTAGTCCAGAGTCCAGGTTCCCGGGTGGTCCACATGTTGTCGCCAACCTCACC 1137
DB 403 ATTCGTAGTCCAGAGTCCAGGTTCCCGGGTGGTCCACATGTTGTCGCCAACCTCACC 344

QY 1138 TGGCTCAATGTTGTCATCAACCTGCTCTATGAGCGCATGAGCCGCAATTCGCCCAA 1197
DB 343 TGGCTCAATGTTGTCATCAACCTGCTCTATGAGCGCATGAGCCGCAATTCGCCCAA 284

QY 1198 GCATATGGCTCCATTTTAAAGAGGCGCCCGAGTTTCCATAGGTTCCATTAAGAACTGT 1257
DB 283 GCATATGGCTCCATTTTAAAGAGGCGCCCGAGTTTCCATAGGTTCCATTAAGAACTGT 224

QY 1258 GACCTAGTACAGAGATTGAGACTGTCCTCCAGGACCAAGTGGC 1306
DB 223 GACCTAGTACAGAGATTGAGACTGTCCTCCAGGACCAAGTGGC 175

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```

RESULT 10
BM726245 660 bp mRNA linear EST 01-MAR-2002
LOCUS
DEFINITION UI-E-EJ0-aih-k-10-0-UI.r1 UI-E-EJ0 Homo sapiens cdna clone
ACCESSION BM726245
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 660)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

```

Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.reagen.com).

The following repetitive elements were found in this cdna
sequence: 599-657, >AT-rich#low_complexity (matched complement)
Seq primer: M13 Reverse.

FEATURES

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Location/Qualifiers
1..660
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-aih-k-10-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stages="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/notes="Organ: eye; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ0 is a subtracted cdna library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cdna synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cdna was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cdna contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGAATAGCGA; eye anterior segment,
AATGCCCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene discovery in the
Visual System, supported by National Eye Institute (NEI)."
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ORIGIN

```

Query Match      36.2%; Score 475; DB 12; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.7e-109;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 832 CCAGTCAGTGTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGAGACGAG 891
DB 1 CCAGTCAGTGTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGAGACGAG 60

QY 892 ATCACACAGAGAGCTATGCAGATGCAGAGAAAGCCCTCCAGAGCATCTGCCAAA 951
DB 61 ATCACACAGAGAGCTATGCAGATGCAGAGAAAGCCCTCCAGAGCATCTGCCAAA 120

QY 952 GCCCAGCCCAATTAAGAGGAGCCAGAGAGCTCCGGATTTTCATCGGAATTTGGGAAGTG 1011
DB 121 GCCCAGCCCAATTAAGAGGAGCCAGAGAGCTCCGGATTTTCATCGGAATTTGGGAAGTG 180

QY 1012 ACTCGAATGTTTTGCTGTGTTCTCTGTTTGCCTGAGCTACATCCCTTCTTCTG 1071
DB 181 ACTCGAATGTTTTGCTGTGTTCTCTGTTTGCCTGAGCTACATCCCTTCTTCTG 240

QY 1072 CTCACATCTTCGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAAC 1131
DB 241 CTCACATCTTCGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAAC 300

QY 1132 CTCACCTGGCTCAATGTTGATCAACCTGTGCTCTATGAGCCATGACCCGCAATTC 1191
DB 301 CTCACCTGGCTCAATGTTGATCAACCTGTGCTCTATGAGCCATGACCCGCAATTC 360

QY 1192 CGCCAAAGCATATGCTCCATTTTAAAGAGGGGCGCCGGAGTTTCCATAGCTCCATAG 1251
DB 361 CGCCAAAGCATATGCTCCATTTTAAAGAGGGGCGCCGGAGTTTCCATAGCTCCATAG 420

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QY 1252 AACTGTGACCTAGTCAACAGAAATTCAGGACTGTCTCTCCAGGACCAAGTGGC 1306
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Db 421 AACTGTGACCTAGTCAACAGAAATTCAGGACTGTCTCTCCAGGACCAAGTGGC 475
|||||
RESULT 11
LOCUS BX336527 1201 bp mRNA linear EST 02-MAY-2003
DEFINITION BX336527 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1029YB18 5-PRIME, mRNA sequence.
ACCESSION BX336527
VERSION BX336527.1 GI:30341523
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6847.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1029BC09QPlkcluster=6847.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1029BC09QPl.
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1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1029YB18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

QY 49 TTAGCCTCTATCATGT-GGAACAGCTCTG-ACGCCAACTTCTCTGCTACC--ATGAGTC 104
|||||
Db 88 TCAGCCTCTATCATGTGCGGAAGCTCTGTACGCCAAATTTCTCTGCTACCTATGGAGTC 147
|||||
QY 105 TGTGCT-GGGCTATCGTTATGTTGCACTAGCTGGGGGTGGTGGCTGTGACAGGCA 163
|||||
Db 148 TGTGCTGGGCTAGCGTTATGTTGCACTAGCTGGGGGTGGTGGCTGTGACAGGNA 207
|||||
QY 164 CCGTGGCAATGTCTCACCTACTGGCCTTG-GCCATCAGCCCAAGTCCGTACCCGA 222
|||||
Db 208 CCGTGGCAATGTCTCAMCMTACTGGCCTTGTGGCATCCAGCCCAAGTCCGTACCCGA 267
|||||
QY 223 TTC--AACCTGCTATAGCAACCTCACCTGCTGAT-----CTCCTCTACTGACGCT 275
|||||
Db 268 TTCTAATCTGCTCATAGGCAACCTCACGACTGTGCTGATGCTACTCTAATGACGCT 327
|||||
QY 276 C---CTTCAGCCCTTCTCTGTGGACACTACCTCCAC-----CTGCACTGGGCGACCGG- 326
|||||
Db 328 CTCTTCTAGCCCTTTTCATGTGGACACTCTACTCTMACCTTGTCTACCTGGGCGACCTGG 387
|||||
QY 327 --TGCCACCTCTGCGAGGATTTGGGCTCCTCCTTTTGGCTCCGAATCTGCTC----- 380
|||||

Db 388 TTGCTACCTTCTGAGGGTATTGGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 447
QY 381 CATCTGACCTCTGCTCTCATCGCACTGGGAGCGTACTCTCTCTCTCTCTCTCTCTCT 440
|||||
Db 448 CCTGTACCTCTGACMTANATMGAAATGGGAGGATAATCTTAATTCANAMMTAGAT 507
|||||
QY 441 TTTTCCCCAAGTTTTCAGTGCCCAAGGGATAGTCTCGCACTGGTGTGAGCACTGGTGTGT 500
|||||
Db 508 TTTTMMNCAAGTTTTCAGTGCCCAAGGGKATAGTCTCTGCACTGTGAGMACCTCKKGTGT 567
|||||
QY 501 GGGGTGGCCAGCTTTGCTCCCTCTCGGCTATTATATCTCTGTAAGTCTGTAAGTCTGAC 560
Db 568 GGGGTGGCCAGCTTTGCTCCCTCTCGGCTATTATATCTCTGTAAGTCTGTAAGTCTGAC 627
QY 561 CTGCACTTTTGACC-GCATCCGAGCGCGGCTTTACACCACTCATCTCTCTCTCTCTCT 618
Db 628 CTTGAGCTTTGACCAGCATCGAGGCGGCTTTACACCACTCATCTCTCTCTCTCTCTCT 687
QY 619 TTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTCTCTCTCTCTCTCTCTCTCT 678
Db 688 TTTGTGCTTGGGCTCASCATTTTGGCATCTTCTATTTCCTCTCTCTCTCTCTCTCTCTCT 747
QY 679 CGAGCAGCAGGCACTGGACCAATACAAAGTTGGCAGAGGCAAGCATCTCTCTCTCTCTCT 738
Db 748 CKAACGACAGGCACTGGACCAATACAAAGTTGGCAGAGGCAAGCATCTCTCTCTCTCTCT 807
QY 739 GTGCCAGGCACTGATGAGGCGCATCCCTGGTGTGTTTCCAGGAGCTGGCAGCAGGTTAGCA 798
Db 808 KTGCCAGCACTGATGAGGCACT--CTTKTCTGTTCCAGGAGCTGGACA-CAGGTTAGCA 864
QY 799 TCAGGAGGCACTGAGGAGGATTTCTATGAGCAGTCTGCTGCTGCCACCACTCTCTCTCTCT 858
Db 865 TCAGGAGGCACTGAGGAGGATTTCTATCTAGGAGCTCTCTCTCTCTCTCTCTCTCTCTCT 919
QY 859 CTGGAAGGGGCACTCATCAGAGTGGGAGACCAAGTCAACCAAGCAAGAGAGAGC 908
Db 920 CTTGAGGAGGCACTCATCAGAGTGGGATGCTTCAATTAATTAATTAATTAATTAATTA 969
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LOCUS BX097926 496 bp mRNA linear EST 04-FEB-2003
DEFINITION BX097926 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGp998215199 ;
IMAGE:2108420, mRNA sequence.
ACCESSION BX097926
VERSION BX097926.1 GI:27829067
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 496)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998215199.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGAAACACATATGAC.
Location/Qualifiers

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:04:24 ; Search time 4851.11 Seconds
(without alignments) 10641.181 Million cell updates/sec

Title: US-10-029-436-1_COPY_61_1251

Perfect score: 1191
Sequence: 1 atgggaacagctctgacgc.....gtttccataggtccattag 1191

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
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32: em.htg.other.*
33: em.htg.mus.*
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35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1191	100.0	1191	6	BD144298	BD144298 Novel G-p
2	1191	100.0	1191	9	AB083586	AB083586 Homo sapi
3	1191	100.0	1433	9	AF237762	AF237762 Homo sapi
4	1191	100.0	1498	6	AR083245	AR083245 Sequence
5	1191	100.0	1535	9	BC020614	BC020614 Homo sapi
6	1191	100.0	1546	6	AX549299	AX549299 Sequence
7	1191	100.0	1546	9	AF282693	AF282693 Homo sapi
8	1191	100.0	1595	6	AX247564	AX247564 Sequence
9	1191	100.0	141003	9	AC078778	AC078778 Homo sapi
10	887.6	74.5	1574	10	BC023249	BC023249 Mus muscu
11	887.6	74.5	207421	2	AC021643	AC021643 Mus muscu
12	886	74.4	1611	10	AF272948	AF272948 Rattus no
13	857.8	72.9	244845	2	AC126846	AC126846 Homo sapi
14	707.6	59.4	141003	2	AC016463	AC016463 Homo sapi
15	87.8	7.4	1382	6	BD229108	BD229108 Endogeneo
16	87.8	7.4	1382	6	AR431783	AR431783 Sequence
17	87.8	7.4	1382	6	AX549134	AX549134 Sequence
18	87.8	7.4	1382	9	AF091890	AF091890 Homo sapi
19	87.8	7.4	1584	6	AR044154	AR044154 Sequence
20	87.8	7.4	1584	6	AR269721	AR269721 Sequence
21	87.8	7.4	1584	6	BD007520	BD007520 Novel his
22	87.8	7.4	1590	9	AY275468	AY275468 Homo sapi
23	87.8	7.4	2400	9	AK122656	AK122656 Homo sapi
24	87.8	7.3	2481	6	BC028163	BC028163 Homo sapi
25	87	7.3	2481	6	AR044088	AR044088 Sequence
26	87	7.3	2481	6	AR091709	AR091709 Sequence
27	87	7.3	2481	6	AX573819	AX573819 Sequence
28	87	7.3	2481	6	BD144779	BD144779 Adrenergi
29	86.2	7.2	1663	6	AX467017	AX467017 Sequence
30	83	7.0	1560	9	HUMALAR	I31773 Human alpha
31	83	7.0	1738	6	AR030765	AR030765 Sequence
32	83	7.0	1738	6	AR088757	AR088757 Sequence
33	83	7.0	1738	6	AR101770	AR101770 Sequence
34	83	7.0	1738	6	I26009	I26009 Sequence 3
35	83	7.0	1738	6	I30002	I30002 Sequence 3
36	83	7.0	1738	6	I83625	I83625 Sequence 3
37	83	7.0	1738	6	AR228241	AR228241 Sequence
38	83	7.0	1738	6	AR270839	AR270839 Sequence
39	83	7.0	1738	6	AR373863	AR373863 Sequence
40	83	7.0	1738	6	AX136023	AX136023 Sequence
41	83	7.0	1738	6	AX137520	AX137520 Sequence
42	83	7.0	1738	9	HSU03865	U03865 Human adren
43	83	7.0	1786	6	AX548750	AX548750 Sequence
44	83	7.0	2669	9	HUMADRENA	M9589 Homo sapien
45	83	7.0	8727	9	AC127458	AC127458 Homo sapi

ALIGNMENTS

RESULT 1
BD144298
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

BD144298
Novel G-protein coupled receptors.
BD144298
BD144298.1 GI:27850056
JP 2002112793-A/23.
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1191)
Haga, T., Takeda, S. and Miyake, N.
Novel G-protein coupled receptors
Patent: JP 2002112793-A 23 16-APR-2002;

Pred. No. is the number of results predicted by chance to have a

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LVPVCTGSPRIAREPTTILMGIFYVLGSSVGFYCLHROVKRAAALDQYKLR
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HRLH"

ORIGIN

Query Match 100.0%; Score 1191; DB 9; Length 1191;
Best Local Similarity 100.0%; Pred. No. 1.2e-299; Indels 0; Gaps 0;
Matches 1191; Conservative 0; Mismatches 0;

Qy	1	ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT	60
Db	1	ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT	60
Qy	61	TATGTTGCAAGTAGCTGGGGGTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC	120
Db	61	TATGTTGCAAGTAGCTGGGGGTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC	120
Qy	121	ACCTACTGCTTGGCCATCCAGCCCAAGCTCCGTACCAGATCAACCTGCTCATAGCC	180
Db	121	ACCTACTGCTTGGCCATCCAGCCCAAGCTCCGTACCAGATCAACCTGCTCATAGCC	180
Qy	181	AACCTCACACTGGTGAATCTCTACTACGACGCTCTTACGCTTCTCTGTGACACC	240
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Qy	241	TACCTCCACTGCACGGCGACCGGTGCCACTTCTGCAGGATATTTGGGCTCCCTT	300
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Qy	301	TTTGGCTCCAAATCTCTCTCACTCTGACACCTCTGCTCATCGCACTGGGAGCTACCTC	360
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Qy	421	CTGGTACGACCTGGGTGTGGGCGTGGCGAGCTTTGCTCCCTCTGGGCTATTTATATC	480
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Qy	541	ATCCTCATGGGCTTACTTTGCTTGGCTGGCTCAGCAGTGTGGATCTTCTATTGCTTC	600
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Qy	661	AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTTCCAGGAG	720
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Qy	721	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCACTCTGAGCCAGTCACT	780
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Qy	781	GCTGCCACCAACCCAGACCTCTGAGGGGACTCATCAGAAAGTGGGACCAAGATCAACAGC	840
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Qy	841	AAGAGACTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTCCAAAGCCCAAGCA	900
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Qy	1081	CTCAATGGTTCATCAACCTGCTTATGACGCCATGAACGCCAATTTCCGCCAAGCA	1140
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Qy	1141	TATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG	1191
Db	1141	TATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG	1191

RESULT 3	AF237762	1493 bp	mRNA	linear	PRI 06-APR-2001
LOCUS	AF237762				
DEFINITION	Homo sapiens orphan G protein-coupled receptor 84 (GPR84) mRNA, complete cds.				
ACCESSION	AF237762				
VERSION	AF237762.1	GI:12711470			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1493)				
TITLE	Wittenberger, T., Schaller, H.C. and Hellebrand, S.				
JOURNAL	An expressed sequence tag (EST) data mining strategy succeeding in the discovery of new G-protein coupled receptors				
MEDLINE	J. Mol. Biol. 307 (3), 799-813 (2001)				
PUBMED	21172992				
REFERENCE	2 (bases 1 to 1493)				
AUTHORS	Wittenberger, T. and Hellebrand, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-MAR-2000) ZMNH, Institut fuer Entwicklungsneurobiologie, Martinistr. 52, Hamburg 20246, Germany				
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ORIGIN

Query Match 100.0%; Score 1191; DB 9; Length 1493;
Best Local Similarity 100.0%; Pred. No. 1.2e-299; Mismatches 0; Indels 0; Gaps 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAAACAGCTCTGACGCAACTTCTCTGTACCATGAGTCTGTGTGGGCTATCGT 60
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QY 61 TATGTTCCAGTTAGCTGGGGGTGGTGGTGTGTGACAGCACCCTGGGCAATGTGCTC 120
DB 129 TATGTTCCAGTTAGCTGGGGGTGGTGGTGTGTGACAGCACCCTGGGCAATGTGCTC 188
QY 121 ACCCTACTGGCTTGGGCATCCAGCCCAAGCTCCGTATCCCGAATCAACCTGCTCATAGCC 180
DB 189 ACCCTACTGGCTTGGGCATCCAGCCCAAGCTCCGTATCCCGAATCAACCTGCTCATAGCC 248
QY 181 AACCTACAGTGGTGTATCTCTCTACTGACAGCTCTCTTACGCCCTTCTGTGTGGACACC 240
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DB 489 CTGGTGAGCACTGGGCTGTGGCGTGCCAGCTTTGCTCCCTCTGGCCTATTTATATC 548
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DB 729 AGCATCCACTCCACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTTCCAGGAG 788
QY 721 CTGGACAGCAGGTTAGCATCAGAGGACCCAGTGTAGGGGATTTTCATCTGAGCCAGTCACT 780
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QY 781 GCTGCCACCCACAGCTCTGGAAGGGGACTCATCAGAGTGGGAGACAGATCAACAGC 840
DB 849 GCTGCCACCCACAGCTCTGGAAGGGGACTCATCAGAGTGGGAGACAGATCAACAGC 908
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DB 1089 CTGGATGCGAGATCCAGGCTCCCGGGTGTGCACATGCTTGTGCAACCTCACCTGG 1148
QY 1081 CTCAATGTTGTCATCAACCTGTGCTCTATGAGCATGAACCCCAATTCCGCCAAGCA 1140
DB 1149 CTCAATGTTGTCATCAACCTGTGCTCTATGAGCATGAACCCCAATTCCGCCAAGCA 1208
QY 1141 TATGCTCCATTTTAAAGAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
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RESULT 4
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DEFINITION Sequence 1 from patent US 5976834.
ACCESSION AR083245
VERSION AR083245.1 GI:10010035
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1498)
AUTHORS Sathie,G.Madhusudan., Fuetterer,W.S., Bergsma,D.John. and Ellis,C.
TITLE cDNA clone HNFJDL5 that encodes a novel human 7-transmembrane receptor
JOURNAL Patent: US 5976834-A 1 02-NOV-1999;
FEATURES
Location/Qualifiers
source 1. 1498
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ORIGIN
Query Match 100.0%; Score 1191; DB 6; Length 1498;
Best Local Similarity 100.0%; Pred. No. 1.2e-299;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAAACAGCTCTGAGCCCAACTTCTCTGTCTACCATGAGTCTGTGGGCTATCGT 60
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DB 136 TATGTTGAGTTAGTGTGGGGGTGGTGGTGTGACAGCACCCTGGGCAATGTGCTC 195
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RESULT 5
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 LOCUS
 DEFINITION Homo sapiens G protein-coupled receptor 84, mRNA (cdna clone
 MGC:22224 IMAGE:4279185), complete cds.
 ACCESSION BC020614
 VERSION BC020614.1 GI:18089044
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1535)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, J., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shchepochko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Snailus, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 12477932
 2 (bases 1 to 1535)
 Strausberg, R.
 Direct Submission
 Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC) Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdepaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 35 Row: K Column: 17
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9968838.

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ORIGIN

Query Match 100.0%; Score 1191; DB 9; Length 1535;
Best Local Similarity 100.0%; Pred. No. 1.2e-299;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAAACAGCTCTGACGCAAACTTCTCTGTACCATGAGTCTGTGGGCTATCGT 60
DB 101 ATGTGGAAACAGCTCTGACGCAAACTTCTCTGTACCATGAGTCTGTGGGCTATCGT 160
QY 61 TATGTTGAGTTAGTCTGGGGGTGGTGGTGTGTGACAGGCAACCGTGGGCAATGTGCTC 120
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LOCUS Sequence 584 from Patent WO02061087.
DEFINITION
ACCESSION AX549299
VERSION AX549299.1 GI:25813960
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
Burmer, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 584 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
Location/Qualifiers
1..1546
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ORIGIN
Query Match 100.0%; Score 1191; DB 6; Length 1546;
Best Local Similarity 100.0%; Pred. No. 1.2e-299;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 91 ATGTGGAAACAGCTCTGACGCAAACTTCTCTGTACCATGAGTCTGTGGGCTATCGT 150
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QY 421 CTGTGAGACACTGGGTTGTGGGGTGGGCGTGGCAGCTTTGCTCCCTCTGCGCTATTTATATC 480
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LOCUS
DEFINITION Homo sapiens inflammation-related G protein-coupled receptor EX33
ACCESSION AF282693
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Yousefi,S., Cooper,P., Potter,S., Mueck,B., and Jarai,G.
TITLE Cloning and expression analysis of a novel G-protein-coupled
JOURNAL J. Leukoc. Biol. 69 (6), 1045-1052 (2001)
MEDLINE 21297471
PUBMED 11404393
REFERENCE
AUTHORS Yousefi,S., Cooper,P., Mueck,B., Potter,S. and Jarai,G.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-2000) NHRC, Wimbleshurst, Horeham, West Sussex
RH12 5AB, UK
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ORIGIN
Query Match 100.0%; Score 1191; DB 9; Length 1546;
Best Local Similarity 100.0%; Pred. No. 1.2e-299;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGAAACAGCTCTGACGCAACTTCTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
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DEFINITION Homo sapiens 12 BAC RP11-968A15 (Roswell Park Cancer Institute
AC078778
VERSION AC078778.34 GI:23307958
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 141003)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-ouman, F.R., Allen, C.,
Alsbrooks, S.L., Amarantunga, H.C., Are, J.R., Ayale, M., Banks, P.,
Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
Buck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chu, D., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Covey, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
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Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S.,
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Frantz, P., Gabisa, A., Gao, J., Garcia, A., Garner, T., Garza, N.,
Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Han, J., Harris, K., Harris, K., Hart, M., Havlak, P.,
Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M.,
Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S.,
Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y.,
Johnson, R., Jolivet, S., Joudan, S., Karlsson, E., Kelly, S., Khan, U.,
King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N.,
Leal, B., Lee, E., Lewis, L., Lewis, L., Li, J., Li, Z., Lichtarge, O.,
Lieu, C., Liu, J., Liu, W., Loulseg, H., Lozano, R.J., Lu, X.,
Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P.,
Marandel, I., Martin, R., Martindale, A., Martinez, E., Massey, E.,
Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S.,
Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T.,
Mohabbat, K., Montgomery, K.I., Morgan, M., Morris, S., Moser, M.,
Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokwkw, S., Ogih, M., Okwuonu, G.,
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scharrer, S., Scott, G., Shen, H., Shim, C., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonaike, I., Sparks, A., Stanley, H., Stone, H., Tang, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Zucherlapat, R.,
Weinstock, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 141003)
Worley, K.C.

REFERENCE
JOURNAL
TITLE
AUTHORS
Direct Submission
Submitted (03-AUG-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

REFERENCE
JOURNAL
TITLE
AUTHORS
Direct Submission
Submitted (27-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

REFERENCE
JOURNAL
TITLE
AUTHORS
Direct Submission
Submitted (25-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

REFERENCE
JOURNAL
TITLE
AUTHORS
Direct Submission
Submitted (25-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

AUTHORS
TITLE
JOURNAL
COMMENT

Worley, K.C.
Direct Submission
Submitted (21-FEB-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 25, 2002 this sequence version replaced gi:22477001.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URU:
<http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht>
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STS		18111..18242 /standard_name="NIB1371"
STS		18229..18400 /standard_name="A002C47"
STS		18349..18457 /standard_name="RH78595"
STS		19062..19158 /standard_name="D12S1927"
STS		71395..71512 /standard_name="Bdya3g12"
STS		77459..77710 /standard_name="D11S2560"
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STS		84170..84320 /standard_name="RH44735"
STS		/standard_name="D12S1994"


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AC021643

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 DEFINITION Mus musculus chromosome 15 clone RP23-169K7 strain C57BL6/J,
 WORKING DRAFT SEQUENCE, 23 unordered pieces.

ACCESSION

AC021643 GI:15143422

HTG; HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 207421)

Grills, G., Han, J., Montgomery, K.T., Lee, E., Long, J., Pomerantz, R.,

Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M.

and Kucherlapati, R.

High throughput Mouse Sequencing

Unpublished

2 (bases 1 to 207421)

Grills, G., Han, J., Montgomery, K.T., Lee, E., Long, J., Pomerantz, R.,

Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M.

and Kucherlapati, R.

Direct Submission

Submitted (19-JAN-2000) Department of Molecular Genetics, Albert

Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,

Bronx, NY 10461, USA

On Aug 9, 2001 this sequence version replaced gi:14717145.

-----Genome Center

Center: Harvard Partners Genome Center

Center Code: HPGC

Web site: <http://www.hpcg.org/Sequence/mouse.html>Contact: hpgc@mendel.mgh.harvard.edu

-----Summary Statistics

Center project name: AAT

Sequencing vector: pUC18; L08752

Chemistry: Dye-terminator Big Dye; 100*

*Consensus quality: 193187 at least Q20

*Consensus quality: 190826 at least Q30

*Consensus quality: 186718 at least Q40

*Estimated insert size: agarose-PP - N/A

*Estimated insert size: 206981 - sum-of-contigs

Quality coverage: agarose-PP - N/A

Quality coverage: 6.5 x in Q20 bases; sum-of-contigs estimation

-----NOTES: This is a 'working draft' sequence. It currently

* consists of 23 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will

* be preserved.

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* 38325 68273: contig of 29949 bp in length

* 68274 68293: gap of unknown length

* 68294 83009: contig of 20716 bp in length

* 83010 83029: gap of unknown length

* 83030 108492: contig of 19463 bp in length

* 108493 108513: gap of unknown length

* 108513 120232: contig of 11720 bp in length

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* 120233 120252: gap of unknown length
* 120253 131080: contig of 10828 bp in length
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* 131101 142689: contig of 11589 bp in length
* 142690 142709: gap of unknown length
* 142710 155481: contig of 12772 bp in length
* 155482 155501: gap of unknown length
* 155502 164014: contig of 8513 bp in length
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* 179423 179442: gap of unknown length
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* 204910 204929: gap of unknown length
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* 207198 207421: contig of 224 bp in length.

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FEATURES

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LOCUS Mus musculus orphan G protein-coupled receptor 84 (Gpr84); mRNA,
complete cds.
ACCESSION AF272948
VERSION AF272948.1 GI:12711474
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Wittenberger,T., Schaller,H.C. and Hellebrand,S.
AUTHORS An expressed sequence tag (EST) data mining strategy succeeding in
TITLE the discovery of new G-protein coupled receptors
J. Mol. Biol. 307 (3), 799-813 (2001)
MEDLINE 21172992
PUBMED 11273702
REFERENCE 2. (bases 1 to 1611)
AUTHORS Wittenberger,T. and Hellebrand,S.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2000) ZMNH, Institut fuer
Entwicklungsneurobiologie, Martinistr. 52, Hamburg 20246, Germany
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Steinle, M., Strong, R., Sutton, A., Satek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission

TITLE
JOURNALREFERENCE
JOURNALAUTHORS
JOURNALTITLE
JOURNALREFERENCE
JOURNALAUTHORS
JOURNALTITLE
JOURNAL

COMMENT

Unpublished
2 (bases 1 to 244845)

Worley, K.C. Submission

Direct Submission

Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 244845)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (03-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Sep 10, 2002 this sequence version replaced gi:21722958.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of MedicineCenter code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: hgsc-help@bcm.tmc.edu----- Project Information
Center project name: GD7A

Center clone name: CH230-11W7

----- Summary Statistics
Assembly program: Phrap; version 0.990329

Consensus quality: 222716 bases at least Q40

Consensus quality: 225022 bases at least Q30

Consensus quality: 226487 bases at least Q20

Estimated insert size: 247241; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).* This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
been provided by the submitter.* This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

* 1 244845: contig of 244845 bp in length.

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DEFINITION AC016463
ACCESSION AC016463
VERSION AC016463.3 GI:7144792
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 141003)
Biren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-1009
Unpublished
2 (bases 1 to 141003)
Baldwin,J., Biren,B., Becker,R., Boguslavsky,L., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A.,
Cooke,P., Dearlano,K., Dewar,K., Domino,M., Donelan,D., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lecoczek,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:6910791.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIPR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3130
Center clone name: 10_O_9
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* NOTE: This record contains 152 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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RESULT 15	BD229108	1382 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD229108				
DEFINITION	Endogenous, constitutively activated protein G-coupled orphan receptor.				
ACCESSION	BD229108				
VERSION	BD229108.1	GI:33038878			
KEYWORDS	JP 2002521681-A/20.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 1382)				
AUTHORS	Behan,D.P., Chalmers,D.T., Liaw,C., Lin,I.L., Lowitz,K. and Chen,R.				
TITLE	Endogenous, constitutively activated protein G-coupled orphan receptor				
JOURNAL	Patent: JP 2002521681-A 20 16-JUL-2002;				

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ARENA PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002521681-A/20
PD 16-JUL-2002
PF 30-JUL-1999 JP 2000562393
PR 31-JUL-1998 US 60/094879,30-OCT-1998 US 60/106300 PR
O4-DEC-1998 US 60/110906,26-FEB-1999 US 60/121851 PI
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LOWITZ,
PI RUOPING CHEN
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CC Description of Artificial Sequence: Synthetic Sequence PH
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:02:34 ; Search time 537.426 Seconds
(without alignments)
9414.519 Million cell updates/sec

Title: US-10-029-436-1_COPY_61_1251

Perfect score: 1191

Sequence: 1 atgtggaacagctctgaagc.....gtttccataggctccattag 1191

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5747725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1191	100.0	1546	7	Abt17029 Human MP2
7	1191	100.0	1546	7	Abz42551 Human G p
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9	1191	100.0	1595	4	Aah78712 Human EX3
10	1191	100.0	2046	4	Aas28996 Genomic s
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23	1154.4	96.9	1416	4	Aak77579 Human imm

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28	346.2	29.1	347	4	AAK60376	Aak60376 Human imm
29	345.4	29.0	483	4	AAS28939	Aas28939 cDNA enco
30	345.4	29.0	483	4	AAS30167	Aas30167 DNA enco
31	345.4	29.0	483	4	AAS34782	Aas34782 cDNA enco
32	345.4	29.0	483	4	AAI99575	Aai99575 Human exp
33	345.4	29.0	483	4	ABA06396	AbA06396 Human cDN
34	345.4	29.0	483	4	ABK43453	AbK43453 DNA enco
35	345.4	29.0	483	5	AAS29521	Aas29521 Human end
36	345.4	29.0	483	6	ABT07774	AbT07774 Novel hum
37	345.4	29.0	483	6	ABV83733	Abv83733 Human pol
38	345.4	29.0	483	7	ACD01422	Adc01422 Human pol
39	345.4	29.0	483	9	ADC45940	Adc45940 Human neo
40	87.8	7.4	1382	3	AAZ51461	Aaz51461 Human G p
41	87.8	7.4	1382	7	ADA19230	Ada19230 Human ins
42	87.8	7.4	1382	7	ABZ42815	Abz42815 Human G p
43	87.8	7.4	1382	8	ADB67667	Adb67667 Human G-p
44	87.8	7.4	1584	2	AAV37701	Aav37701 Human his
45	87.8	7.4	1584	7	ACA55686	Aca55686 Signallin

ALIGNMENTS

RESULT 1

ABZ42892

ID ABZ42892 standard; DNA; 1191 BP.

XX AC ABZ42892;

XX DT 06-MAR-2003 (first entry)

XX DE Human GPCR polynucleotide SEQ ID NO 45.

XX KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;

XX KW drug development; gustatory; taste; fragrance; gene; ds.

XX OS Homo sapiens.

XX PN WO200216548-A2.

XX PD 28-FEB-2002.

XX PF 30-JUL-2001; 2001WO-IB001446.

XX PR 04-AUG-2000; 2000JP-00237818.

XX PR 13-FEB-2001; 2001JP-00034434.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Haga T, Takeda S, Mitaku S;

XX WPI, 2002-304118/34.

XX P-Psdb; ABP95618.

Database global search for G protein-coupled receptors, proteins and

encoded genes for studying in vivo signal transduction mechanism and

identifying targets for drug development.

XX Claim 9; SEQ ID NO 45; 97pp + Sequence Listing; Japanese.

XX The invention relates to a method for screening G protein-coupled

receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-

ABP95942) by extracting open-reading frames containing 6-8 transmembrane

domains with 250-1000 amino acid residues to give a gene homologous with

a known GPCR gene. The receptor proteins and encoded genes are useful for

studying in vivo signal transduction mechanism and identifying targets in

form of agonists and antagonists by screening intrinsic and extrinsic

ligands as bitter taste inhibitors, taste enhancers and fragrance

CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1191 BP; 242 A; 370 C; 294 G; 285 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1191; DB 6; Length 1191;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGGAACAGCTGTGACGCAACTTCTCTGTCTACCATGAGTGTGCTATCGT 60
 DB 1 ATGTGGAACAGCTGTGACGCAACTTCTCTGTCTACCATGAGTGTGCTATCGT 60
 QY 61 TATGTTGAGTTAGCTGGGGGTGTGGTGTGTGACAGCCAGCGTGGCAATGTGCTC 120
 DB 61 TATGTTGAGTTAGCTGGGGGTGTGGTGTGTGACAGCCAGCGTGGCAATGTGCTC 120
 QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGTCTATAGCC 180
 DB 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGTCTATAGCC 180
 QY 181 AACCTCAGACTGGTGTATCTCTCTACTACGACGCTCTTACGCGCTTCTGTGAGACCC 240
 DB 181 AACCTCAGACTGGTGTATCTCTCTACTACGACGCTCTTACGCGCTTCTGTGAGACCC 240
 QY 241 TACCTCCACCTGCACTGGCGCAGCCGCTGACACCTTCTGACGGGTATTTGGGCTCTCTT 300
 DB 241 TACCTCCACCTGCACTGGCGCAGCCGCTGACACCTTCTGACGGGTATTTGGGCTCTCTT 300
 QY 301 TTTGCTTCCAAATTCGTCTCATCTGACGCTCTGCTCATCTGCACTGGACGCTACCTC 360
 DB 301 TTTGCTTCCAAATTCGTCTCATCTGACGCTCTGCTCATCTGCACTGGACGCTACCTC 360
 QY 361 CTCATTGCCCCACCTTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGGATAGTGTGGCA 420
 DB 361 CTCATTGCCCCACCTTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGGATAGTGTGGCA 420
 QY 421 CTGTGAGCACTGGGTGTGGGCTGGCGAGCTTGTCTCCCTCTGGCCTATTATATC 480
 DB 421 CTGTGAGCACTGGGTGTGGGCTGGCGAGCTTGTCTCCCTCTGGCCTATTATATC 480
 QY 481 CTGTGAGCACTGGGTGTGGGCTGGCGAGCTTGTCTCCCTCTGGCCTATTATATC 540
 DB 481 CTGTGAGCACTGGGTGTGGGCTGGCGAGCTTGTCTCCCTCTGGCCTATTATATC 540
 QY 541 ATCTCTATGGGCACTACTTTGTGCTTGGGCTGAGCACTGTGGCATTTCTATTGCTC 600
 DB 541 ATCTCTATGGGCACTACTTTGTGCTTGGGCTGAGCACTGTGGCATTTCTATTGCTC 600
 QY 601 ATCCACGCCAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 660
 DB 601 ATCCACGCCAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 660
 QY 661 AGCATCCACTCCAACTTGGCCAGGCTGATGAGGCTGCTGCTGCTTCCAGGAG 720
 DB 661 AGCATCCACTCCAACTTGGCCAGGCTGATGAGGCTGCTGCTGCTTCCAGGAG 720
 QY 721 CTGACAGCAGGTTAGCATCAGGAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAG 780
 DB 721 CTGACAGCAGGTTAGCATCAGGAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAG 780
 QY 781 GCTCCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 840
 DB 781 GCTCCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 840
 QY 841 AAGAGAGCTAAGCAGAGTGGCAGAGAAAGCCCTCCAGAGCATCTGCGAAAGCCAGCCA 900
 DB 841 AAGAGAGCTAAGCAGAGTGGCAGAGAAAGCCCTCCAGAGCATCTGCGAAAGCCAGCCA 900
 QY 901 ATTAAGGAGCCAGAGAGCTCCGAGTCTTTCATCGGAATTTGGGAGGTGACTCCGAATG 960
 DB 901 ATTAAGGAGCCAGAGAGCTCCGAGTCTTTCATCGGAATTTGGGAGGTGACTCCGAATG 960

QY 961 TGTTTGTGCTGCTTCTCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTCTCTCAACATT 1020
 DB 961 TGTTTGTGCTGCTTCTCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTCTCTCAACATT 1020
 QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGTGTCACATGCTTGTGCAACCTCACCTGG 1080
 DB 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGTGTCACATGCTTGTGCAACCTCACCTGG 1080
 QY 1081 CTCATGTTGCTATCAACCTGCTGCTCTATGAGCCATGACCGCAATTCGCGCAAGCA 1140
 DB 1081 CTCATGTTGCTATCAACCTGCTGCTCTATGAGCCATGACCGCAATTCGCGCAAGCA 1140
 QY 1141 TATGCTCCATTTTAAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
 DB 1141 TATGCTCCATTTTAAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
 RESULT 2.
 AAI68793
 ID AAI68793 standard; cDNA; 1227 BP.
 XX
 AC AAI68793;
 XX DT 22-JAN-2002 (first entry)
 XX DE Human MAR1 cDNA fragment.
 XX KW MAR1; monoamine receptor-1; human; cytostatic; gene therapy; tumour;
 XX KW psychiatric disorder; transgenic animal; knockout animal; ss.
 XX OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 19..1209
 FT /tag= a
 FT /product= "MAR1"
 XX DE10021474-A1.
 XX PD 08-NOV-2001.
 XX PD 03-MAY-2000; 2000DE-01021474.
 XX PR 03-MAY-2000; 2000DE-01021474.
 XX (BRUE/) BRUES M.
 XX (BOEN/) BOENISCH H.
 XX Bruess M, Boenisch H;
 XX WPI; 2002-011956/02.
 XX P-PSDB; AAG80225.
 XX
 PT New monoamine receptor-1 gene, MAR1, useful for diagnosis and treatment
 PT of MAR1-related diseases.
 XX
 PS Disclosure; Page 4; 6pp; German.
 XX
 CC This invention describes a novel human monoamine receptor-1 (MAR1) gene
 CC (I) which has cytosolic activity and can be used for gene therapy. (I),
 CC and derived (anti)sense oligonucleotides, are useful in treatment and
 CC diagnosis of (I)-related diseases (possibly tumours and psychiatric
 CC disorders), for producing transgenic/knockout animals, and for
 CC recombinant expression of the protein (II) that it encodes. (II) is
 CC useful in ligand-binding studies and screening assays, also for treatment
 CC and diagnosis of (II)-related diseases. This sequence encodes the human
 CC MAR1 monoamine receptor-1 protein
 XX
 SQ Sequence 1227 BP; 249 A; 383 C; 299 G; 296 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1191; DB 6; Length 1227;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGTGGAACAGCTGTGACGCCAACCTTCCTCTCTACCATGAGCTGTGTGCTGGGCTATCGT	60		
Db	19	ATGTGGAACAGCTGTGACGCCAACCTTCCTCTCTACCATGAGCTGTGTGCTGGGCTATCGT	78		
QY	61	TATGTTGCAGTTAGCTGGGGGTGGTGGGCTGTGACAGGACCGTGGGCAATGTGCTC	120		
Db	79	TATGTTGCAGTTAGCTGGGGGTGGTGGGCTGTGACAGGACCGTGGGCAATGTGCTC	138		
QY	121	ACCCTACTGGCCTTGCCATCCAGCCCAAGCTCCGTACCAGATCAACCTGCTCATAGCC	180		
Db	139	ACCCTACTGGCCTTGCCATCCAGCCCAAGCTCCGTACCAGATCAACCTGCTCATAGCC	198		
QY	181	AACCTCAGCTGGCTGATCTCTCTACTGACAGCTCCCTCAGCCCTTCTCTGGACACC	240		
Db	199	AACCTCAGCTGGCTGATCTCTCTACTGACAGCTCCCTCAGCCCTTCTCTGGACACC	258		
QY	241	TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCTT	300		
Db	259	TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCTT	318		
QY	301	TTTGCCCTCOAATCTGTCTCTCATCTGACCTCTGCTCATCGACCTGGAGGCTACCTC	360		
Db	319	TTTGCCCTCOAATCTGTCTCTCATCTGACCTCTGCTCATCGACCTGGAGGCTACCTC	378		
QY	361	CTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA	420		
Db	379	CTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA	438		
QY	421	CTGGTGAGCACTGGGTTGTGGGCTGGCCAGCTTTGCTCCCTCTGGGCTATTTATATC	480		
Db	439	CTGGTGAGCACTGGGTTGTGGGCTGGCCAGCTTTGCTCCCTCTGGGCTATTTATATC	498		
QY	481	CTGGTACTGTAGTCTGCACTGCACTGTTGACCGCATCCGAGCGCGGCTTACACACC	540		
Db	499	CTGGTACTGTAGTCTGCACTGCACTGTTGACCGCATCCGAGCGCGGCTTACACACC	558		
QY	541	ATCCTCATGGGCACTTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC	600		
Db	559	ATCCTCATGGGCACTTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC	618		
QY	601	ATCCACCGCAGGTCAAAACAGCAGACACAGGCACTGGACCAATACAGTTGGACAGCA	660		
Db	619	ATCCACCGCAGGTCAAAACAGCAGACACAGGCACTGGACCAATACAGTTGGACAGCA	678		
QY	661	AGCATCCACTCCAAACCATGTGGCCAGACTGTAGTGGCCATGCTGTGCTTCCAGAG	720		
Db	679	AGCATCCACTCCAAACCATGTGGCCAGACTGTAGTGGCCATGCTGTGCTTCCAGAG	738		
QY	721	CTGGACAGAGGTTAGCATCAGAGGACCCAGTGGAGGATTTCACTGAGCCAGTCACT	780		
Db	739	CTGGACAGAGGTTAGCATCAGAGGACCCAGTGGAGGATTTCACTGAGCCAGTCACT	798		
QY	781	GCTGCCACCAACCCAGACCTGGAGGGGACTCATCAGAGTGGAGCCAGATCAACAGC	840		
Db	799	GCTGCCACCAACCCAGACCTGGAGGGGACTCATCAGAGTGGAGCCAGATCAACAGC	858		
QY	841	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCCGCCA	900		
Db	859	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCCGCCA	918		
QY	901	ATTAAGAGCCAGAGAGCTCCGATCTTCTATCGGAATTTGGGAAGTGACTCGAATG	960		
Db	919	ATTAAGAGCCAGAGAGCTCCGATCTTCTATCGGAATTTGGGAAGTGACTCGAATG	978		
QY	961	TGTTTTGCTGTCT	1020		
Db	979	TGTTTTGCTGTCT	1038		
QY	1021	CTGGATGCCAGATCCAGGCTCCCGGGTGGTCCACATGCTGTCTGCCAACTCACCTGG	1080		
Db	1039	CTGGATGCCAGATCCAGGCTCCCGGGTGGTCCACATGCTGTCTGCCAACTCACCTGG	1098		

QY	1081	CTCANTGTTGCATCAACCTGTCTCTATGACGCGCATGAACCGCAATTCGCCAAGCA	1140		
Db	1099	CTCANTGTTGCATCAACCTGTCTCTATGACGCGCATGAACCGCAATTCGCCAAGCA	1158		
QY	1141	TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG	1191		
Db	1159	TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG	1209		
RESULT 3					
ID	ACC84331	standard; DNA; 1311 BP.			
XX	ACC84331;				
AC	ACC84331;				
XX	03-OCT-2003 (first entry)				
DE	Human hp15a receptor coding sequence.				
KW	Human; hp15a; receptor; G-protein coupled receptor; cardiant;				
XX	gastrointestinal; gene therapy; gene; ds.				
OS	Homo sapiens.				
Key	Location/Qualifiers				
FT	61..1251				
CDS	/*tag= a				
FT	/product= "hp15a"				
XX	WO2003054540-A1.				
PN	03-JUL-2003.				
XX	19-DEC-2002; 2002WO-US040612.				
PF	19-DEC-2001; 2001US-00029436.				
PR	(SYNA-) SYNAPTIC PHARM CORP.				
XX	Smith KE, Weinschank R;				
PI	WPI: 2003-559173/52.				
DR	P-FSDB; ABR52422.				
DR	New recombinant nucleic acid, useful for preparing a composition for				
PT	treating disorders linked to human hp15a receptor e.g. cardiovascular or				
PT	gastrointestinal disorders.				
XX	Claim 1; Fig 1A-B; 98pp; English.				
PS	The present sequence is that of nucleic acid encoding a human orphan G-				
XX	protein coupled receptor, designated hp15a. The sequence was initially				
CC	identified in a human placenta genomic library using probes representing				
CC	transmembrane domains III, V and VI of human serotonin 5-Hy1Dbeta				
CC	receptor. The endogenous ligand for hp15a is likely to be a				
CC	neuromodulator since the receptor is present in several regions of the				
CC	human brain. The invention provides hp15a nucleic acids, vectors, host				
CC	cells, antibodies, probes, antisense oligonucleotides, transgenic non-				
CC	human animals, methods of isolating the receptor, methods of treating an				
CC	abnormality that is associated with activity of hp15a e.g. cardiovascular				
CC	or gastrointestinal disorders, and methods of determining binding of				
CC	compounds to hp15a				
XX	Sequence 1311 BP; 266 A; 409 C; 315 G; 321 T; 0 U; 0 Other;				
SQ	Query Match 100.0%; Score 1191; DB 8; Length 1311;				
	Best Local Similarity 100.0%; Pred. No. 0;				
	Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	ATGTGGACAGCTGTGACGCCAACCTTCTCTGCTACCATGAGTGTGTGCTGGGCTATCGT	60		
Db	61	ATGTGGACAGCTGTGACGCCAACCTTCTCTGCTACCATGAGTGTGTGCTGGGCTATCGT	120		

QY 61 TATGTTGAGTTAGTCTGGGGGGTGGTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC 120
 Db 121 TATGTTGAGTTAGTCTGGGGGGTGGTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC 180
 QY 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGTCGTTACCGGATTCACCTGCTCATAGCC 180
 Db 181 ACCCTACTGGCTTGGCCATCCAGCCCAAGTCGTTACCGGATTCACCTGCTCATAGCC 240
 QY 181 AACCTACACTGGCTGTCTCTCTACTGACAGCTCTCTTCAAGCCCTTCTCTGTGGACACC 240
 Db 241 AACCTACACTGGCTGTCTCTCTACTGACAGCTCTCTTCAAGCCCTTCTCTGTGGACACC 300
 QY 241 TACCTCCACTGCTGACCTGGCCAGCCGCTGACCTCTCTGACGGTATTTGGGCTCCTCCTT 300
 Db 301 TACCTCCACTGCTGACCTGGCCAGCCGCTGACCTCTCTGACGGTATTTGGGCTCCTCCTT 360
 QY 301 TTTGCTCTCCAAATCTGTCTCATCTCTGACCTCTCTGCTCATGCGCTGACCTGCGCTACCTC 360
 Db 361 TTTGCTCTCCAAATCTGTCTCATCTCTGACCTCTCTGCTCATGCGCTGACCTGCGCTACCTC 420
 QY 361 CTCATTGCCCACTTAACTTTTCCCAAGTTTTCAGTCCCAAGGGATAGTGTGCGCA 420
 Db 421 CTCATTGCCCACTTAACTTTTCCCAAGTTTTCAGTCCCAAGGGATAGTGTGCGCA 480
 QY 421 CTGCTGAGCACTGGGTGTGGGGTGGCCAGCTTTGCTCCCTCTGGCCCTATTTTATATC 480
 Db 481 CTGCTGAGCACTGGGTGTGGGGTGGCCAGCTTTGCTCCCTCTGGCCCTATTTTATATC 540
 QY 481 CTGCTGAGCACTGGGTGTGGGGTGGCCAGCTTTGCTCCCTCTGGCCCTATTTTATATC 540
 Db 541 CTGCTGAGCACTGGGTGTGGGGTGGCCAGCTTTGCTCCCTCTGGCCCTATTTTATATC 600
 QY 541 ATCTCTCATGGCACTTCTTGTCTTGGCTGAGCACTGCTGCTCTCTTCTTCTTATTCCTC 600
 Db 601 ATCTCTCATGGCACTTCTTGTCTTGGCTGAGCACTGCTGCTCTCTTCTTCTTATTCCTC 660
 QY 601 ATCCACCGCCAGTCAACAGCAGCAGCAGCAGCTGACCAATACAGTTTGGACAGGCA 660
 Db 661 ATCCACCGCCAGTCAACAGCAGCAGCAGCAGCTGACCAATACAGTTTGGACAGGCA 720
 QY 661 AGCATCCACTCCACCTGCTGCGCAGCAGTGTGAGGCTGCTGCTGCTTTCACAGGAG 720
 Db 721 AGCATCCACTCCACCTGCTGCGCAGCAGTGTGAGGCTGCTGCTGCTTTCACAGGAG 780
 QY 721 CTGACAGCAGCTTATGATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCACT 780
 Db 781 CTGACAGCAGCTTATGATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCACT 840
 QY 781 GCTGCCACCCAGCAGCTTGGAGGGGATCATCAGAGTGGGAGCAGCAGTCAACAGC 840
 Db 841 GCTGCCACCCAGCAGCTTGGAGGGGATCATCAGAGTGGGAGCAGCAGTCAACAGC 900
 QY 841 AAGAGAGTAAAGAGTGGCAGAGAAAGCCCTCCAGAGCATCTGCAAGCCAGCCAGCA 900
 Db 901 AAGAGAGTAAAGAGTGGCAGAGAAAGCCCTCCAGAGCATCTGCAAGCCAGCCAGCA 960
 QY 901 ATTAAGAGCAGCAGAGCTCCGATTTCTTCATCGGAATTTGGGAAGTGTGCTGGAATG 960
 Db 961 ATTAAGAGCAGCAGAGCTCCGATTTCTTCATCGGAATTTGGGAAGTGTGCTGGAATG 1020
 QY 961 TGTCTTCTGTTCTCTCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 Db 1021 TGTCTTCTGTTCTCTCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 QY 1021 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 Db 1081 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 1081 CTCAATGGTTGCATCAACCTGTGCTATGACAGCAGTGAACCGCAATTCGCCAGCA 1140
 Db 1141 CTCAATGGTTGCATCAACCTGTGCTATGACAGCAGTGAACCGCAATTCGCCAGCA 1200

QY 1141 TATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
 Db 1201 TATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1251

RESULT 4
 AAV38513
 ID AAV38513 standard; cDNA; 1498 BP.
 XX
 AC AAV38513;
 XX
 DT 07-OCT-1998 (first entry)
 XX
 Human 7-transmembrane receptor encoding cDNA clone HNFJD15.
 DE
 XX
 G-protein coupled receptor; HNFJD15; treatment; diagnosis; infection;
 KW HIV-1; HIV-2; cancer; screening; human; 7-transmembrane receptor;
 KW Parkinson's disease; vaccine; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 76..1266
 FT /*tag= a
 FT /product= "human 7-transmembrane receptor, HNFJD15"
 FT
 XX BP853125-A2.
 XX
 PD 15-JUL-1998.
 XX
 PF 20-NOV-1997; 97EP-00309347.
 XX
 PR 09-JAN-1997; 97US-00775428.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Sathe GW, Fuettner WS, Bergsma DJ, Ellis C;
 XX
 DR WPI; 1998-364650/32.
 DR P-PSDB; AAW62598.
 XX
 PT Human G-protein coupled receptor, HNFJD15 - used e.g. in treatment and
 PT diagnosis of infections e.g. by HIV-1, HIV-2 and cancers and screening of
 PT antagonistic or agonistic compounds.
 XX
 PS Claim 4; Fig 1; 19pp; English.
 XX
 CC This cDNA encodes a human 7-transmembrane receptor, HNFJD15. HNFJD15 is a
 CC human G-protein coupled receptor and are used in vaccines to protect
 CC mammals from infections e.g. bacterial, fungal, protozoan and viral
 CC infections (especially infections caused by HIV-1 or HIV-2), cancers and
 CC Parkinson's disease. The HNFJD15 polypeptides can be used to produce
 CC antibodies which are used to treat such infections, isolate or identify
 CC clones expressing the polypeptide or to purify the polypeptide. The
 CC polypeptides can also be used to screen for compounds binding to,
 CC activating or inhibiting activation of HNFJD15. They can be used to
 CC diagnose diseases and susceptibility to diseases related to expression or
 CC activity of HNFJD15
 XX
 SQ Sequence 1498 BP; 346 A; 438 C; 349 G; 365 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1191; DB 2; Length 1498;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTGTGAGCCAACTTCTCTGTCTACCATGATGTGTGCTGGGCTATCGT 60
 Db 76 ATGTGGAACAGCTGTGAGCCAACTTCTCTGTCTACCATGATGTGTGCTGGGCTATCGT 135
 QY 61 TATGTTGAGTTAGTCTGGGGGGTGGTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC 120
 Db 136 TATGTTGAGTTAGTCTGGGGGGTGGTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC 195

121 ACCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCCGATTCAACCTGCTCATAGCC 180
 196 ACCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCCGATTCAACCTGCTCATAGCC 255
 181 AACCTACACTGGCTGATCTCTCTACTGCGAGCTCCCTTACGCGCTTCTCTGAGACAC 240
 256 AACCTACACTGGCTGATCTCTCTACTGCGAGCTCCCTTACGCGCTTCTCTGAGACAC 315
 241 TACCTCCACTGCATGGCGCCACCGGTGGCCACCTTCTGCGAGGATATTGGGCTCTCCTT 300
 316 TACCTCCACTGCATGGCGCCACCGGTGGCCACCTTCTGCGAGGATATTGGGCTCTCCTT 375
 301 TTGCGCTCAATCTGCTCTCACTCTGACCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 360
 376 TTGCGCTCAATCTGCTCTCACTCTGACCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 435
 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGCTGCA 420
 436 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGCTGCA 495
 421 CTGGTGAGACCTGGGTGTTGGCGTGGCGAGCTTGTCCCTCTGGCGCTATTATATC 480
 496 CTGGTGAGACCTGGGTGTTGGCGTGGCGAGCTTGTCCCTCTGGCGCTATTATATC 555
 481 CTGGTACCTGTAGTCTGCACTCTGCACTTTGACCGCATCCGAGCGCGCTTACACCAAC 540
 556 CTGGTACCTGTAGTCTGCACTCTGCACTTTGACCGCATCCGAGCGCGCTTACACCAAC 615
 541 ATCCTCATGGGCACTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 616 ATCCTCATGGGCACTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
 601 ATCCACCGCAGCTCAAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 660
 676 ATCCACCGCAGCTCAAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 735
 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCGCATCGCTGCTGCTGCTGCTG 720
 736 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCGCATCGCTGCTGCTGCTGCTG 795
 721 CTGGCAGCAGGTTAGCATCAGGAGACCGAGTGGGATTTCTCTGAGCAGCTCAGT 780
 796 CTGGCAGCAGGTTAGCATCAGGAGACCGAGTGGGATTTCTCTGAGCAGCTCAGT 855
 781 GCTGCCACCCAGCAGCAGCTCCGATTTCTTATCGGAATTTGGGAAGTGAATCAACAGC 840
 856 GCTGCCACCCAGCAGCAGCTCCGATTTCTTATCGGAATTTGGGAAGTGAATCAACAGC 915
 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTCCAAAGCCAGCA 900
 916 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTCCAAAGCCAGCA 975
 901 ATTAAAGGAGCCAGAGAGCTCCGATTTCTTATCGGAATTTGGGAAGTGAATCAACAG 960
 976 ATTAAAGGAGCCAGAGAGCTCCGATTTCTTATCGGAATTTGGGAAGTGAATCAACAG 1035
 961 TGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 1036 TGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1095
 1021 CTGGATCCAGAGTCCAGGCTCCCGGTGGTCCACATGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 1096 CTGGATCCAGAGTCCAGGCTCCCGGTGGTCCACATGCTGCTGCTGCTGCTGCTGCTGCTG 1155
 1081 CTCATGGTTGATCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 1156 CTCATGGTTGATCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1215
 1141 TATGGCTCCATTTTAAAGAGGCGCCCGAGTTTCCATAGGCTCCATTAG 1191
 1216 TATGGCTCCATTTTAAAGAGGCGCCCGAGTTTCCATAGGCTCCATTAG 1266

RESULT 5
 AAS98070
 ID AAS98070 standard; DNA; 1546 BP.
 XX
 AC AAS98070;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human DNA for potential G protein-coupled receptor #27.
 XX
 KW Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; asthma;
 KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;
 KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
 KW depression; epilepsy; macular degeneration; lymphoma; melanoma;
 KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
 KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
 KW tuberculois; cognition disorder; memory disorder; anorexia;
 KW hormonal release disorder; cardiovascular activity disorder;
 KW pain perception disorder; obesity; diabetes; diabetes; obesity; diabetes;
 KW hyperlipidaemia; stroke; gene therapy.
 XX
 KW Homo sapiens.
 OS
 XX WO200185791-A1.
 XX
 PD 15-NOV-2001.
 XX
 PF 11-MAY-2001; 2001WO-US015332.
 XX
 PR 11-MAY-2000; 2000US-0203217P.
 PR 18-MAY-2000; 2000US-0205945P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Brown JP, Miller M, Burner G, Fabre-Suver C, Pritchard D;
 XX WPI; 2002-066595/09.
 XX
 PT Novel G protein-coupled receptor polypeptides including galanin receptor
 PT polypeptides useful for identifying modulators that are useful for
 PT treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,
 PT stroke.
 XX
 PS Disclosure; Page 130-131; 144pp; English.
 XX
 CC The invention relates to an isolated polypeptide encoded by a nucleic
 CC acid molecule that is at least 80% identical to the G protein-coupled
 CC (GPCR) polynucleotides included in the specification. Also included are
 CC probes based on the GPCR sequences (including antisense probes), a host
 CC cell comprising an expression vector comprising the GPCR sequence,
 CC antibodies raised against the polypeptides, and methods of identifying
 CC modulators of the polypeptides. The polypeptides are useful for
 CC identifying modulator compounds which function as modulators, activators,
 CC repressors, agonists or antagonists of the novel GPCR polypeptides
 CC including the GAL4 polypeptide. The antibodies and nucleic acid probes as
 CC described above can be used to detect the presence of the polypeptides
 CC and nucleic acids and are used to diagnose a variety of diseases or
 CC disorders in which GPCRs are involved e.g., Alzheimer's disease, basal cell
 CC amyotrophic lateral sclerosis, asthma, atherosclerosis, epilepsy,
 CC carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic
 CC obstructive pulmonary disease, Crohn's disease, depression, psoriasis,
 CC macular degeneration, lymphoma, melanoma, multiple sclerosis,
 CC osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid
 CC arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other
 CC diseases listed in the specification. The probes and antibodies are also
 CC useful for diagnosing cognition and memory disorders, anorexia, hormonal
 CC release disorders, cardiovascular activity disorders, pain perception
 CC disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds
 CC that decrease or increase the expression of galanin receptor (GAL4) can
 CC be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR
 CC nucleic acid is useful for treating the above mentioned disorders by gene
 CC therapy techniques. The present sequence is a novel GPCR polynucleotide

Query Match	100.0%;	Score 1191;	DB 7;	Length 1546;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1191;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTCTGCTGGGCTATCGT	60	
DB	91	ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTCTGCTGGGCTATCGT	150	
QY	61	TATGTTGCAGTTAGCTTGGGGGGTGTGTGGTGTGACAGGCCACCGTGGGCAATGTCTC	120	
DB	151	TATGTTGCAGTTAGCTTGGGGGGTGTGTGGTGTGACAGGCCACCGTGGGCAATGTCTC	210	
QY	121	ACCTTACTGGCTTGGGCCATCAGAGCCAAAGTCCGTACCGGATTCAACCTGCTCATAGCC	180	
DB	211	ACCTTACTGGCTTGGGCCATCAGAGCCAAAGTCCGTACCGGATTCAACCTGCTCATAGCC	270	
QY	181	AACCTCACACTGGCTGATCTCCTTACTGACGCTCTTCAAGCCCTCTCTGFGGCAACC	240	
DB	271	AACCTCACACTGGCTGATCTCCTTACTGACGCTCTTCAAGCCCTCTCTGFGGCAACC	330	
QY	241	TACCTCCAGCTGACCTGGGGGACCGGTGCCACCTCTGAGGGTATTGCGGCTCCCTT	300	
DB	331	TACCTCCAGCTGACCTGGGGGACCGGTGCCACCTCTGAGGGTATTGCGGCTCCCTT	390	
QY	301	TTTGCTCCAAATCTGTCTCCATPCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC	360	
DB	391	TTTGCTCCAAATCTGTCTCCATPCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC	450	
QY	361	CTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGGATAGTCTGGCA	420	
DB	451	CTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGGATAGTCTGGCA	510	
QY	421	CTGGTGAGCACTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC	480	
DB	511	CTGGTGAGCACTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC	570	
QY	481	CTGGTACTGTAGCTTGCACTCGAGCTTTTGACCGCATCGAGGCGCGCTTACACCAAC	540	
DB	571	CTGGTACTGTAGCTTGCACTCGAGCTTTTGACCGCATCGAGGCGCGCTTACACCAAC	630	
QY	541	ATCCTCATGGGATCTACTTTGTGTTGGCTCAGCAGTGTTCGGCATCTTCTATTGGCTC	600	
DB	631	ATCCTCATGGGATCTACTTTGTGTTGGCTCAGCAGTGTTCGGCATCTTCTATTGGCTC	690	
QY	601	ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGGCAAGGCA	660	
DB	691	ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGGCAAGGCA	750	
QY	661	AGCATCCACTCCAAACATGTGGCCAGGACTGATGAGGCAATGCTGTGCTTTCCAGGAG	720	
DB	751	AGCATCCACTCCAAACATGTGGCCAGGACTGATGAGGCAATGCTGTGCTTTCCAGGAG	810	
QY	721	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT	780	
DB	811	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT	870	
QY	781	GCTGGCAACCAACGAGACCTTGGAAGGGGACTCATCAGAAGTGGGAGACAGATCAACAGC	840	
DB	871	GCTGGCAACCAACGAGACCTTGGAAGGGGACTCATCAGAAGTGGGAGACAGATCAACAGC	930	
QY	841	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCACGCCA	900	
DB	931	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCACGCCA	990	
QY	901	ATTAAAGAGCCAGAGAGTCCGGATTTCTTCATTCGGAAATTTGGGAAGGTGACTCGAATG	960	
DB	991	ATTAAAGAGCCAGAGAGTCCGGATTTCTTCATTCGGAAATTTGGGAAGGTGACTCGAATG	1050	
QY	961	TGTTTTGCTGTGTTCCCTTGTGCTTGGCCCTGAGGCTACATCCCTTCTTGTGCTCAACATT	1020	
DB	1051	TGTTTTGCTGTGTTCCCTTGTGCTTGGCCCTGAGGCTACATCCCTTCTTGTGCTCAACATT	1110	
QY	1021	CTGGAATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGTTGTGTGCCAACCTCACCTGG	1080	

Db	1111	CTGATGCGCAGAGTCCAGGCTCCCGGGTGGTCCCATGCTTGTCGCAACCTCACCTGG	1170
Qy	1081	CTCAATGGTTGCATCAACCTGCTCTATGACGCGATGAACCGCAATTCGCGCAAGCA	1140
Db	1171	CTCAATGGTTGCATCAACCTGCTCTATGACGCGATGAACCGCAATTCGCGCAAGCA	1230
Qy	1141	TATGGCTCCCATTTTAAAGAGAGGGCCCGGAGTTTCCATAGGTTCCATTAG	1191
Db	1231	TATGGTCCCATTTTAAAGAGAGGGCCCGGAGTTTCCATAGGTTCCATTAG	1281
RESULT 7			
ABZ42551			
ID	ABZ42551	standard; DNA; 1546 BP.	
XX	ABZ42551;		
XX			
DT	04-MAR-2003	(first entry)	
XX			
DE	Human G protein-coupled receptor	EX33 nucleotide SEQ ID NO:584.	
XX			
KW	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;		
KW	G protein-coupled receptor modulator; antibody; immune-related disease;		
KW	Growth-related disease; cell regeneration-related disease; AIDS; cancer;		
KW	immunological-related cell proliferative disease; autoimmune disease;		
KW	Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;		
KW	osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;		
KW	graft versus host disease; Parkinson's disease; multiple sclerosis; pain;		
KW	psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;		
KW	mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;		
KW	hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;		
KW	ulcer; gene; ds.		
OS			
XX	Homo sapiens.		
XX			
PN	W0200261087-A2.		
XX			
PD	08-AUG-2002.		
XX			
XX	19-DEC-2001; 2001WO-US050107.		
PF			
XX			
PR	19-DEC-2000; 2000US-0257144P.		
XX			
XX	(LIFE-) LIFESPAN BIOSCIENCES INC.		
FA			
XX			
PI	Burmer GC, Roush CL, Brown JP;		
XX			
XX	WPI: 2003-046718/04.		
DR	P-PSDB; ABP81705.		
DR			
XX	New isolated antigenic peptides e.g., for G protein-coupled receptors		
PT	(GPCR), useful for diagnosing and designing drugs for treating conditions		
PT	in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or		
PT	autoimmune diseases.		
XX			
XX	Disclosure; Fig 1; 523pp; English.		
PS			
XX			
CC	The present invention describes antigenic peptides (I) comprising: (a)		
CC	any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino		
CC	acids. Also described: (1) an assay for the detection of a particular G		
CC	protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;		
CC	and (2) an isolated antibody having high specificity and high affinity or		
CC	avidity for a particular GPCR. (I) can be used as GPCR modulators and in		
CC	gene therapy. The antigenic peptides for GPCRs are useful in detecting an		
CC	antibody against a particular GPCR, and in the production of specific		
CC	antibodies. The peptides and antibodies are also useful for detecting the		
CC	presence or absence of corresponding GPCRs. The antigenic peptides for		
CC	GPCRs and antibodies are useful for diagnosing and designing drugs for		
CC	treating immune-related diseases, growth-related diseases, cell		
CC	regeneration-related disease, immunological-related cell proliferative		
CC	diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,		
CC	atherosclerosis, bacterial, fungal protozoan or viral infections,		

Disclosure: Fig 1; 523pp; English.

The present invention describes antigenic peptides (1) comprising: (a) any one of 1601 sequences (see APP2019 to APP3619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections,

CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which qPCR are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1546 BP; 383 A; 442 C; 351 G; 370 T; 0 U; 0 Other;

Query Match 100.0%; Score 1191; DB 7; Length 1546;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAGACAGCTGTGACGCAACTTCTCTGCTACCATGAGTGTGCTGGGCTATCGT 60
 Db |||||
 QY 91 ATGTGGAGACAGCTGTGACGCAACTTCTCTGCTACCATGAGTGTGCTGGGCTATCGT 150
 Db |||||
 QY 61 TATGTTGCAGTTAGCTGGGGGTTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC 120
 Db |||||
 QY 151 TATGTTGCAGTTAGCTGGGGGTTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC 210
 QY 121 ACCCTACTGGCTTGGGCAATCCAGCCCAAGTCCGTACCCGATTCACCTGCTCATAGCC 180
 Db |||||
 QY 211 ACCCTACTGGCTTGGGCAATCCAGCCCAAGTCCGTACCCGATTCACCTGCTCATAGCC 270
 QY 181 AACCTCACACTGGCTGATCTCTCTACTGTGACAGCTCTCTTTCAGCCCTTCTCTGTGGACACC 240
 Db |||||
 QY 271 AACCTCACACTGGCTGATCTCTCTACTGTGACAGCTCTCTTTCAGCCCTTCTCTGTGGACACC 330
 QY 241 TACCTCACACTGGCTGATCTCTCTACTGTGACAGCTCTCTTTCAGCCCTTCTCTGTGGACACC 300
 Db |||||
 QY 331 TACCTCACACTGGCTGATCTCTCTACTGTGACAGCTCTCTTTCAGCCCTTCTCTGTGGACACC 390
 QY 301 TTTCCCTCCAACTTCT 360
 Db |||||
 QY 391 TTTCCCTCCAACTTCT 450
 QY 361 CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGGGATGCTGGCA 420
 Db |||||
 QY 451 CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGGGATGCTGGCA 510
 QY 421 CTGGTGAGCACTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGGCTATTTATATC 480
 Db |||||
 QY 511 CTGGTGAGCACTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGGCTATTTATATC 570
 QY 481 CTGGTGAGCACTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGGCTATTTATATC 540
 Db |||||
 QY 571 CTGGTGAGCACTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGGCTATTTATATC 630
 QY 541 ATCTGTATGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTCTATTCCTC 600
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 QY 631 ATCTGTATGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTCTATTCCTC 690
 QY 601 ATCCACCGCCAGGTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660
 Db |||||
 QY 691 ATCCACCGCCAGGTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 750
 QY 661 AGCATCAGCTCCAACTTGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 720
 Db |||||
 QY 751 AGCATCAGCTCCAACTTGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 810
 QY 721 CTGGACAGCAGGTTAGCATCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
 Db |||||
 QY 811 CTGGACAGCAGGTTAGCATCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 870
 QY 781 GCTGCCACCAACCCAGCCCTGGGAGGGGATCTCATAGAGTGGGAGCAGCAGCAGCAGCAGCAGCAGCAG 840
 Db |||||
 QY 871 GCTGCCACCAACCCAGCCCTGGGAGGGGATCTCATAGAGTGGGAGCAGCAGCAGCAGCAGCAGCAGCAG 930

QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 900
 Db |||||
 QY 931 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 990
 QY 901 ATTAAGAGAGCCAGAGAGCTCCGGAATCTTCATCGGNAATTTGGAGAGTGCATCGAATG 960
 Db |||||
 QY 991 ATTAAGAGAGCCAGAGAGCTCCGGAATCTTCATCGGNAATTTGGAGAGTGCATCGAATG 1050
 QY 961 TGTGTTGCTGTTGCT 1020
 Db |||||
 QY 1051 TGTGTTGCTGTTGCT 1110
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 Db |||||
 QY 1111 CTGGATGCGCAGATCCAGGCTCCCGGGTGTGTGCATGCTTGTGCAACCTCACCTGG 1170
 QY 1081 CTCAATGTTGTCATCAACCCCTGTCTCTATGAGCCATGAACCCCAATTCGGCCAAAGCA 1140
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 QY 1171 CTCAATGTTGTCATCAACCCCTGTCTCTATGAGCCATGAACCCCAATTCGGCCAAAGCA 1230
 QY 1141 TATGCTCCATTTTAAAGAGGGCCCGAGTTCATAGGCTCCATTAG 1191
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 QY 1231 TATGCTCCATTTTAAAGAGGGCCCGAGTTCATAGGCTCCATTAG 1281

RESULT 8

AAI199548
 ID AAI199548 standard; cDNA; 1579 BP.
 XX AC AAI199548;
 XX XX
 DT 04-JAN-2002 (first entry)
 XX DE Human expressed polynucleotide SEQ ID NO 11.
 XX Human; neutropenic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnary;
 KW antiparkinsonian; antiscikling; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatocytic; cerebroprotective; antineoplastic; antitumor;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; caradant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
 XX OS Homo sapiens.
 XX PN WO200155387-A1.
 XX XX
 PD 02-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US001310.
 XX PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184684P.
 PR 02-MAR-2000; 2000US-0186350P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465573/50.
XX P-PSDB; AAM99936.
XX Isolated digestive system associated polypeptide for treating, preventing
PT and/or prognosing disorders related to the digestive system including
PT digestive system cancers and also for testing and detection e.g.
PT diagnosis.
XX Claim 1; SEQ ID NO 11; 509pp + Sequence Listing; English.
XX The invention relates to novel genes (AAM99548-AAM99604) and proteins
CC (AAM99936-AAM99984) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (anti)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences

XX	Sequence	1579 BP; 356 A; 460 C; 381 G; 379 T; 0 U; 3 Other;	
XX	Query Match	100.0%; Score 1191; DB 4; Length 1579;	
XX	Best Local Similarity	100.0%; Pred. No. 0;	
XX	Matches 1191; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGTGGAAAGCTCTGAGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT	60
Db	112	ATGTGGAAAGCTCTGAGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT	171
Qy	61	TATGTTCCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGACCGTGGGCAATGTGCTC	120
Db	172	TATGTTCCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGACCGTGGGCAATGTGCTC	231
Qy	121	ACCTTACCTGCTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGTCTATAGC	180
Db	232	ACCTTACCTGCTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGTCTATAGC	291
Qy	181	AACCTCACCTGCTGATCTCTCTACTGTGACAGCTCTCTCAGCCCTTCTCTGTGGACAC	240
Db	292	AACCTCACCTGCTGATCTCTCTACTGTGACAGCTCTCTCAGCCCTTCTCTGTGGACAC	351
Qy	241	TACCTCACCTGCTGATCTCTCTACTGTGACAGCTCTCTCAGCCCTTCTCTGTGGACAC	300
Db	352	TACCTCACCTGCTGATCTCTCTACTGTGACAGCTCTCTCAGCCCTTCTCTGTGGACAC	411
Qy	301	TTTGCTCCCAATCTGTCTCTGCTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
Db	412	TTTGCTCCCAATCTGTCTCTGCTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	471
Qy	361	CTCATTCGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA	420
Db	472	CTCATTCGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA	531
Qy	421	CTGTGAGCAGCTGGTGTGGGCTGGGCGGAGCTTTGCTCCCTCTGGCTATTTATATC	480
Db	532	CTGTGAGCAGCTGGTGTGGGCTGGGCGGAGCTTTGCTCCCTCTGGCTATTTATATC	591
Qy	481	CTGTGAGCAGCTGGTGTGGGCTGGGCGGAGCTTTGCTCCCTCTGGCTATTTATATC	540
Db	592	CTGTGAGCAGCTGGTGTGGGCTGGGCGGAGCTTTGCTCCCTCTGGCTATTTATATC	651
Qy	541	ATCCTCATGGGCACTACTTTGCTGGCTCAGCAGTGTGGCACTTTCTATTCGCTC	600
Db	652	ATCCTCATGGGCACTACTTTGCTGGCTCAGCAGTGTGGCACTTTCTATTCGCTC	711
Qy	601	ATCCACCGCCAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	660
Db	712	ATCCACCGCCAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	771
Qy	661	AGCATCCACTCCACCACTGTGGCAGGACTGATGAGGCCATGCTGGTGGTTCCTCAGGAG	720
Db	772	AGCATCCACTCCACCACTGTGGCAGGACTGATGAGGCCATGCTGGTGGTTCCTCAGGAG	831
Qy	721	CTGGACAGCAGGTTAGCATCAGAGGACCCAGTGGGAGTTTTCATCTGAGCCAGTCACT	780
Db	832	CTGGACAGCAGGTTAGCATCAGAGGACCCAGTGGGAGTTTTCATCTGAGCCAGTCACT	891
Qy	781	GCTGCCACCCAGGACCTCCGAGGAGTCTATCAGAGTGGGAGCAGATCAACAGC	840
Db	892	GCTGCCACCCAGGACCTCCGAGGAGTCTATCAGAGTGGGAGCAGATCAACAGC	951
Qy	841	AAGAGCCTAAGCAGTGGCAGAGAAAGCCCTCCAGAGCAGTCTGCCAAGCCAGGCA	900
Db	952	AAGAGCCTAAGCAGTGGCAGAGAAAGCCCTCCAGAGCAGTCTGCCAAGCCAGGCA	1011
Qy	901	ATTAAAGGAGCAGAGAGCTCCGGATTCTTCTATCGAAATTTGGGAGGTTGACTCGAATG	960
Db	1012	ATTAAAGGAGCAGAGAGCTCCGGATTCTTCTATCGAATTTGGGAGGTTGACTCGAATG	1071
Qy	961	TGTTTCTGTGTTCTCTCTGCTTGGCTGAGCTATATCCCTTCTGCTGTCAACATT	1020

Db	1072	TGTTTGTGTTGTTCTCTCTGCTTTGCCCTGAGCTACATCCCTTCTGCTGCTCAACATT	1131
Qy	1021	CTGGATGCCAGAGTCCAGGCTCCCGGGTGTGCATGCTGTGCTGCAACCTCAGCTGG	1080
Db	1132	CTGGATGCCAGAGTCCAGGCTCCCGGGTGTGCATGCTGTGCTGCAACCTCAGCTGG	1191
Qy	1081	CTCATGTTTCATCAACCCCTGCTCTATGACGCTGACCCGCAATTCGCGCAAGCA	1140
Db	1192	CTCAATGTTGCTATCAACCCCTGCTCTATGACGCTGACCCGCAATTCGCGCAAGCA	1251
Qy	1141	TATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG	1191
Db	1252	TATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG	1302
RESULT 9			
AAH78712			
ID	AAH78712	standard; cDNA; 1595 BP.	
XX	AAH78712;		
AC	AAH78712;		
XX	29-JAN-2002	(first entry)	
DT	29-JAN-2002	(first entry)	
XX	Human EX33	G-protein coupled receptor cDNA sequence.	
DE	Human EX33	G-protein coupled receptor; EX33; rheumatoid arthritis;	
XX	Human EX33	G-protein coupled receptor; EX33; rheumatoid arthritis;	
KW	Human EX33	neutrophil-associated inflammatory disease; Crohn's disease;	
KW	Human EX33	ulcerative colitis; chronic obstructive pulmonary disease; COPD;	
KW	Human EX33	adult respiratory distress syndrome; ARDS; rheumatoid arthritis;	
KW	Human EX33	inflammatory bowel disease; human; GPCR; ss.	
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	CDS	140..1330	
FT		/*tag= a	
FT		/product= "EX33 protein"	
XX	WO200166597-A2.		
PN	13-SEP-2001.		
PD	05-MAR-2001;	2001WO-EP002462.	
XX	06-MAR-2000;	2000US-00518832.	
PR	(NOVS)	NOVARTIS AG.	
XX	(NOVS)	NOVARTIS-ERFINDUNGEN VERW GES MBH.	
PA	Jarai G,	Cooper PR, Yousefi S;	
PI	WPI;	2001-541917/60.	
DR	Use of an	inflammatory related G-protein coupled receptor (EX33), a	
XX	polynucleotide	encoding it or other compounds (e.g. antibodies) in the	
PT	diagnosis or	treatment of a neutrophil-associated inflammatory disease,	
PT	e.g. rheumatoid	arthritis.	
XX	Claim 3;	Page 29; 32pp; English.	
PS	The present	nucleic acid sequence represents cDNA encoding EX33, a human	
XX	inflammatory	disease-related G-protein coupled receptor (GPCR). G-protein	
CC	coupled	receptors are important targets in therapeutic applications	
CC	because	they are involved in a wide variety of physiological and	
CC	pathological	processes. The invention comprises the use of the EX33	
CC	polypeptide	and polynucleotide in the diagnosis or treatment of a	
CC	neutrophil-	associated inflammatory disease. The EX33 polypeptide, EX33	
CC	polynucleotide,	an antibody specific to the EX33 polypeptide, and an	
CC	antisense	oligonucleotide/polynucleotide probe specific to the EX33	
CC	polynucleotide	are useful in the diagnosis or treatment of neutrophil-	
CC	associated	inflammatory diseases, such as chronic obstructive pulmonary	
CC	disease (COPD),	adult respiratory distress syndrome (ARDS), rheumatoid	
CC	arthritis,	and inflammatory bowel diseases (e.g., Crohn's disease and	

CC ulcerative colitis)

XX Sequence 1595 BP; 393 A; 459 C; 365 G; 378 T; 0 U; 0 Other;

Query Match 100.0%; Score 1191; DB 4; Length 1595;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAATCTCTCTCTACCATGAGTCTGTCTGGCTATCGT 60

Db 140 ATGTGGAACAGCTCTGACGCCAATCTCTCTCTACCATGAGTCTGTCTGGCTATCGT 199

QY 61 TATGTGCAAGTAGCTGGGGGTGGTGGCTGTGACAGCACCCTGGCAATGTGCTC 120

Db 200 TATGTGCAAGTAGCTGGGGGTGGTGGCTGTGACAGCACCCTGGCAATGTGCTC 259

QY 121 ACCCTACTGGCTTGGCCATCCAGGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180

Db 260 ACCCTACTGGCTTGGCCATCCAGGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 319

QY 181 AACCTCAGACTGGCTGATCTCTCTACTGACAGCTCTCTCAGCCCTTCTCTGTGACACC 240

Db 320 AACCTCAGACTGGCTGATCTCTCTACTGACAGCTCTCTCAGCCCTTCTCTGTGACACC 379

QY 241 TACCTCCACTGCACCTGGGGCAACCGGTGCCACTTCTGACGGTATTTGGGCTCTCCTT 300

Db 380 TACCTCCACTGCACCTGGGGCAACCGGTGCCACTTCTGACGGTATTTGGGCTCTCCTT 439

QY 301 TTGGCTCAATCTGTCTCCATCTGACCTCTGCTCTCATCTGCACTGGAGCGTACCTC 360

Db 440 TTGGCTCAATCTGTCTCCATCTGACCTCTGCTCTCATCTGCACTGGAGCGTACCTC 499

QY 361 CTCATTGGCCCACTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGATAGTGTGCA 420

Db 500 CTCATTGGCCCACTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGATAGTGTGCA 559

QY 421 CTGGTGAGCACCTGGGTTTGGCGGTGGCCAGCTTGTCTCCCTCTGGCCTATTATATC 480

Db 560 CTGGTGAGCACCTGGGTTTGGCGGTGGCCAGCTTGTCTCCCTCTGGCCTATTATATC 619

QY 481 CTGGTACTGTAGTCTGACCTCTGACCTTGTACCCGATCCGAGCGCGCTTACACACC 540

Db 620 CTGGTACTGTAGTCTGACCTCTGACCTTGTACCCGATCCGAGCGCGCTTACACACC 679

QY 541 ATCCCTCATGGGATCTACTTTGTCTGGGCTGAGCAGTGTGGCATCTTCTATTGCGCTC 600

Db 680 ATCCCTCATGGGATCTACTTTGTCTGGGCTGAGCAGTGTGGCATCTTCTATTGCGCTC 739

QY 601 ATCCACCGCCAGGTCAAAACGACGACGACGACGACGACGACGACGACGACGACGAC 660

Db 740 ATCCACCGCCAGGTCAAAACGACGACGACGACGACGACGACGACGACGACGACGAC 799

QY 661 AGCATCCACTCCCAACCATGTGGCCAGGACTGATGAGGCCATCGCTGCTTCCAGGAG 720

Db 800 AGCATCCACTCCCAACCATGTGGCCAGGACTGATGAGGCCATCGCTGCTTCCAGGAG 859

QY 721 CTGGACAGCAGGTAGCATCAGGAGCACCAGTGGGGATTTTCATCTGAGCCAGTCACT 780

Db 860 CTGGACAGCAGGTAGCATCAGGAGCACCAGTGGGGATTTTCATCTGAGCCAGTCACT 919

QY 781 GCTGCCACCAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 840

Db 920 GCTGCCACCAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 979

QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTTCCAGAGGATCTGCGCAAGCCAGGCA 900

Db 980 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTTCCAGAGGATCTGCGCAAGCCAGGCA 1039

QY 901 ATTAAAGGAGCAGAGAGCTCCGATTTCTTCTATCGGAATTTGGGAGGTGACTCGAATG 960

Db 1040 ATTAAAGGAGCAGAGAGCTCCGATTTCTTCTATCGGAATTTGGGAGGTGACTCGAATG 1099

QY 961 TGTGTTGCTGTGTTCTCTCTGCTTGGCCCTGACGCTACATCCCTTCTTGTGCTCAACAT 1020

Db 1100 TGTGTTGCTGTGTTCTCTCTGCTTGGCTGAGCTACATCCCTTCTTGTGCTCAACAT 1159

QY 1021 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTCTGTCACACCTCACTGG 1080

Db 1160 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTCTGTCACACCTCACTGG 1219

QY 1081 CTCATGTTGTCATCAACCTGCTCTATGACGACGATGAACGCAATTCGCCCAAGCA 1140

Db 1220 CTCATGTTGTCATCAACCTGCTCTATGACGACGATGAACGCAATTCGCCCAAGCA 1279

QY 1141 TATGGCTCCATTTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1191

Db 1280 TATGGCTCCATTTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1330

RESULT 10

AAS28996

ID AAS28996 standard; DNA; 2046 BP.

XX AC AAS28996;

XX AC AAS28996;

DT 21-NOV-2001 (first entry)

XX Genomic sequence #2 encoding novel human uterine motility polypeptide.

DE Human; uterine motility-association disorder; uterus; pregnancy; labour;

KW menstrual cycle; gene therapy; ds.

XX Homo sapiens.

OS WO200155201-A1.

PN 02-AUG-2001.

PD 17-JAN-2001; 2001WO-US001317.

PF 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225271P.

PR 14-AUG-2000; 2000US-0225275P.

PR 14-AUG-2000; 2000US-0225278P.

PR 14-AUG-2000; 2000US-0225279P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226688P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228294P.

PR	01-SEP-2000;	2000US-0229287P.	PR	17-NOV-2000;	2000US-0249212P.
PR	01-SEP-2000;	2000US-0229343P.	PR	17-NOV-2000;	2000US-0249213P.
PR	01-SEP-2000;	2000US-0229344P.	PR	17-NOV-2000;	2000US-0249214P.
PR	01-SEP-2000;	2000US-0229345P.	PR	17-NOV-2000;	2000US-0249215P.
PR	05-SEP-2000;	2000US-0229509P.	PR	17-NOV-2000;	2000US-0249216P.
PR	05-SEP-2000;	2000US-0229513P.	PR	17-NOV-2000;	2000US-0249217P.
PR	06-SEP-2000;	2000US-0230437P.	PR	17-NOV-2000;	2000US-0249218P.
PR	06-SEP-2000;	2000US-0230438P.	PR	17-NOV-2000;	2000US-0249244P.
PR	08-SEP-2000;	2000US-0231242P.	PR	17-NOV-2000;	2000US-0249245P.
PR	08-SEP-2000;	2000US-0231243P.	PR	17-NOV-2000;	2000US-0249264P.
PR	08-SEP-2000;	2000US-0231244P.	PR	17-NOV-2000;	2000US-0249285P.
PR	08-SEP-2000;	2000US-0231413P.	PR	17-NOV-2000;	2000US-0249297P.
PR	08-SEP-2000;	2000US-0231414P.	PR	17-NOV-2000;	2000US-0249299P.
PR	08-SEP-2000;	2000US-0232080P.	PR	17-NOV-2000;	2000US-0249300P.
PR	08-SEP-2000;	2000US-0232081P.	PR	01-DEC-2000;	2000US-0250160P.
PR	12-SEP-2000;	2000US-0231968P.	PR	01-DEC-2000;	2000US-0250391P.
PR	14-SEP-2000;	2000US-0232372P.	PR	05-DEC-2000;	2000US-0251030P.
PR	14-SEP-2000;	2000US-0232373P.	PR	05-DEC-2000;	2000US-0251988P.
PR	14-SEP-2000;	2000US-0232399P.	PR	05-DEC-2000;	2000US-0256719P.
PR	14-SEP-2000;	2000US-0232400P.	PR	06-DEC-2000;	2000US-0251479P.
PR	14-SEP-2000;	2000US-0232401P.	PR	08-DEC-2000;	2000US-0251856P.
PR	14-SEP-2000;	2000US-0233063P.	PR	08-DEC-2000;	2000US-0251868P.
PR	14-SEP-2000;	2000US-0233064P.	PR	08-DEC-2000;	2000US-0251869P.
PR	14-SEP-2000;	2000US-0233065P.	PR	08-DEC-2000;	2000US-0251989P.
PR	21-SEP-2000;	2000US-0234223P.	PR	08-DEC-2000;	2000US-0251990P.
PR	21-SEP-2000;	2000US-0234274P.	PR	11-DEC-2000;	2000US-0254097P.
PR	25-SEP-2000;	2000US-0234937P.	PR	05-JAN-2001;	2001US-0259678P.
PR	26-SEP-2000;	2000US-0234938P.	XX		
PR	27-SEP-2000;	2000US-0235484P.	PA	(HUMA-) HUMAN GENOME SCI INC.	
PR	27-SEP-2000;	2000US-0235834P.	XX		
PR	27-SEP-2000;	2000US-0235836P.	XX	Rosen CA, Barash SC, Ruben SM;	
PR	29-SEP-2000;	2000US-0236327P.	XX	WPI; 2001-488777/53.	
PR	29-SEP-2000;	2000US-0236367P.	DR		
PR	29-SEP-2000;	2000US-0236368P.	XX		
PR	29-SEP-2000;	2000US-0236369P.	XX		
PR	29-SEP-2000;	2000US-0236370P.	PT	New nucleic acid molecules encoding 49 human secreted proteins for	
PR	02-OCT-2000;	2000US-0236802P.	PT	diagnosing, preventing, treating or ameliorating medical conditions and	
PR	02-OCT-2000;	2000US-0237037P.	PT	used as food additives or preservatives.	
PR	02-OCT-2000;	2000US-0237038P.	XX		
PR	02-OCT-2000;	2000US-0237039P.	XX	Disclosure; SEQ ID NO 130; 524pp; English.	
PR	02-OCT-2000;	2000US-0237040P.	XX		
PR	13-OCT-2000;	2000US-0239935P.	CC	The present invention relates to the isolation of novel human uterine	
PR	13-OCT-2000;	2000US-0239937P.	CC	motility-association polypeptides (AAU18094-AAU18152), and cDNA and	
PR	20-OCT-2000;	2000US-0240960P.	CC	genomic sequences encoding for these polypeptides. The sequences of the	
PR	20-OCT-2000;	2000US-0241221P.	CC	invention are useful in the diagnosis, treatment, prevention and/or	
PR	20-OCT-2000;	2000US-0241785P.	CC	prognosis of diseases associated with uterine motility such as pregnancy	
PR	20-OCT-2000;	2000US-0241786P.	CC	and labour, and menstrual disorders. The polynucleotide sequences of the	
PR	20-OCT-2000;	2000US-0241787P.	CC	invention are also useful in gene therapy. AAS28995-AAS29020 represent	
PR	20-OCT-2000;	2000US-0241809P.	CC	genomic sequences encoding for novel human uterine motility-association	
PR	20-OCT-2000;	2000US-0241826P.	CC	polypeptides. Note: The sequence data for this patent did not form part	
PR	01-NOV-2000;	2000US-0244617P.	CC	of the printed specification, but was obtained in electronic format	
PR	08-NOV-2000;	2000US-0246474P.	CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	
PR	08-NOV-2000;	2000US-0246475P.	XX		
PR	08-NOV-2000;	2000US-0246476P.	SQ	Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;	
PR	08-NOV-2000;	2000US-0246477P.			
PR	08-NOV-2000;	2000US-0246478P.			
PR	08-NOV-2000;	2000US-0246523P.			
PR	08-NOV-2000;	2000US-0246524P.			
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PR	08-NOV-2000;	2000US-0246526P.			
PR	08-NOV-2000;	2000US-0246527P.			
PR	08-NOV-2000;	2000US-0246528P.			
PR	08-NOV-2000;	2000US-0246532P.			
PR	08-NOV-2000;	2000US-0246609P.			
PR	08-NOV-2000;	2000US-0246610P.			
PR	08-NOV-2000;	2000US-0246611P.			
PR	08-NOV-2000;	2000US-0246613P.			
PR	17-NOV-2000;	2000US-0249207P.			
PR	17-NOV-2000;	2000US-0249208P.			
PR	17-NOV-2000;	2000US-0249209P.			
PR	17-NOV-2000;	2000US-0249210P.			
PR	17-NOV-2000;	2000US-0249211P.			

Query Match 100.0%; Score 1191; DB 4; Length 2046;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGACAGCTCTGACGCCAAGCTTCTCTCTGCTACCATGAGTGTGCTGGGCTATCGT 60
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 DB 637 ATGTGGACAGCTCTGACGCCAAGCTTCTCTCTGCTACCATGAGTGTGCTGGGCTATCGT 696
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QY 61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACGACCCGTTGGGCAATGTGCTC 120
 |||||

DB 697 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACGACCCGTTGGGCAATGTGCTC 756
 |||||

QY 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCGTACCGTACCTCACTGCTCATAGCC 180
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DB 757 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCGTACCGTACCTCACTGCTCATAGCC 816
 |||||

QY 181 AACCTCACTGGCTGATCTCTCTACTGACGCTCTCTCAGCCCTTCTCTGTGGACACC 240
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DB 817 AACCTCACTGGCTGATCTCTCTACTGACGCTCTCTCAGCCCTTCTCTGTGGACACC 876
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PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 14-SEP-2000; 2000US-0233066P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234224P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236357P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-488787/53.
 DR New polynucleotides and polypeptides, useful for diagnosing, treating,
 PT preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte
 PT imbalance or neoplastic disorders, autoimmune diseases, cancers.
 XX Claim 1; SEQ ID NO 155; 506pp; English.
 XX The invention relates to novel nucleic acids and polypeptides useful for
 CC diagnosing, treating, preventing and/or prognosing disorders related to
 CC these polypeptides. The polynucleotides are especially useful in the
 CC diagnosis, prognosis, prevention and/or treatment of diseases which
 CC include kidney disorders (e.g. renal failure or nephritis),
 CC cardiovascular disorders (e.g. hypertension or myocardial infarction),
 CC blood disorders (e.g. anaemia or blood coagulation disorders),
 CC electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia),
 CC neoplastic disorders (e.g. nephroma or renal cell cancer), autoimmune
 CC diseases, cancers, inflammatory diseases, reproductive system disorders,
 CC endocrine disorders, neural activity and neurological disorders, wound
 CC healing and respiratory disorders. AAS30165-AAS30251 represent the novel
 CC human renal and cardiovascular-associated nucleic acid sequences of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at: ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1191; DB 4; Length 2046;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGGAACAGCTCTGACGGCAACTTCTCTGTACCATGAGTCTGTGGGCTATCGT 60
 Db 637 ATGTGGAACAGCTCTGACGGCAACTTCTCTGTACCATGAGTCTGTGGGCTATCGT 696
 QY 61 TATGTTGAGTTAGTCTGGGGGTGGTGGTGTGACAGCCACCGTGGGCAATGTCTC 120
 Db 697 TATGTTGAGTTAGTCTGGGGGTGGTGGTGTGACAGCCACCGTGGGCAATGTCTC 756
 QY 121 ACCCTACTGGCCCTTGGCCATCCAGCCCAAGTCGGTACCGGATCAACCTGCTCATAGCC 180
 Db 757 ACCCTACTGGCCCTTGGCCATCCAGCCCAAGTCGGTACCGGATCAACCTGCTCATAGCC 816
 QY 181 AACCTCACCTGGCTGATCTCTTACTGACAGCTCTCTTCTGAGCCCTTCTCTGTGGACAC 240
 Db 817 AACCTCACCTGGCTGATCTCTTACTGACAGCTCTCTTCTGAGCCCTTCTCTGTGGACAC 876
 QY 241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACAGGATATTGGGCTCTCTT 300
 Db 877 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACAGGATATTGGGCTCTCTT 936
 QY 301 TTTGCTTCCCAATTCTGTCTCCATCCCTGACCTCTGCTCATCGCACTGGACGCTACCTC 360
 Db 937 TTTGCTTCCCAATTCTGTCTCCATCCCTGACCTCTGCTCATCGCACTGGACGCTACCTC 996
 QY 361 CTGATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGGGATAGTGTGGCA 420

Db 997 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTTCAGTGCACAGGGATAGTGTGCCA 1056
 QY 421 CTGGTGAGCACCTGGGTTGTGGGGCTGGCCAGCTTTGTCCCTCTGGCCTATTATATC 480
 Db 1057 CTGGTGAGCACCTGGGTTGTGGGGCTGGCCAGCTTTGTCCCTCTGGCCTATTATATC 1116
 QY 481 CTGGTACTGTAGTCTGCACCTGCGAGCTTTGACCCGATCCGAGGCGGCGCTTACACACC 540
 Db 1117 CTGGTACTGTAGTCTGCACCTGCGAGCTTTGACCCGATCCGAGGCGGCGCTTACACACC 1176
 QY 541 ATCCCTCATGGGATCTACTTTCTGTTGGCTCAGCAGTGTGGCATCTTCTATTGCGCTC 600
 Db 1177 ATCCCTCATGGGATCTACTTTCTGTTGGCTCAGCAGTGTGGCATCTTCTATTGCGCTC 1236
 QY 601 ATCCACCGCCAGGTCAACAGCAGCAGCAGCAGGCACTGGACCAATACAAAGTTGGCAGGCA 660
 Db 1237 ATCCACCGCCAGGTCAACAGCAGCAGCAGCAGGCACTGGACCAATACAAAGTTGGCAGGCA 1296
 QY 661 AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCATGCTGGTTCGTTCCAGAG 720
 Db 1297 AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCATGCTGGTTCGTTCCAGAG 1356
 QY 721 CTGGCAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCACT 780
 Db 1357 CTGGCAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCACT 1416
 QY 781 GTTGCACACCCAGCAGCAGTGGAGGGGACTCATCAGAGTGGGAGACAGATCAACAGC 840
 Db 1417 GTTGCACACCCAGCAGCAGTGGAGGGGACTCATCAGAGTGGGAGACAGATCAACAGC 1476
 QY 841 AAGAGAGCTAAGCAGATGCGAGAGAAAGCCCTCCAGAGGATCTGCCAAAGCCCGAGGCA 900
 Db 1477 AAGAGAGCTAAGCAGATGCGAGAGAAAGCCCTCCAGAGGATCTGCCAAAGCCCGAGGCA 1536
 QY 901 ATTAAGAGGAGCAGAGAGCTCCGATTTTCATCGGAATTTGGGAAGTGAAGTCAATG 960
 Db 1537 ATTAAGAGGAGCAGAGAGCTCCGATTTTCATCGGAATTTGGGAAGTGAAGTCAATG 1596
 QY 961 TGTGTTGCTGCTCTCTGCTTTCCTGCTGAGCTACATCCCTCTGCTGCTCAACATT 1020
 Db 1597 TGTGTTGCTGCTCTCTGCTTTCCTGCTGAGCTACATCCCTCTGCTGCTCAACATT 1656
 QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGTTCACATGCTTTGCTGCCAACTCACCTGG 1080
 Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGTTCACATGCTTTGCTGCCAACTCACCTGG 1716
 QY 1081 CTCATGCTTGCATCAACCTCTGCTCTATGAGCCATGAACCCGCAATTCGCGCAAGCA 1140
 Db 1717 CTCATGCTTGCATCAACCTCTGCTCTATGAGCCATGAACCCGCAATTCGCGCAAGCA 1776
 QY 1141 TATGGCTCCATTTTAAAGAGGGGCCCCGAGTTTCCATAGGCTCCATTAG 1191
 Db 1777 TATGGCTCCATTTTAAAGAGGGGCCCCGAGTTTCCATAGGCTCCATTAG 1827
 RESULT 12
 AAS35064
 ID AAS35064 standard; DNA; 2046 BP.
 XX
 AC AAS35064;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE DNA #14 encoding human neoplastic disease associated polypeptide.
 KW Human; neoplastic disease associated polypeptide; cancer; gene therapy;
 KW hyperproliferative disorder; neural disorder; immune system disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ds.
 OS Homo sapiens.

PN
 XX
 PD
 XX
 XX
 PF
 XX
 WO200155163-A1.
 02-AUG-2001.
 17-JAN-2001; 2001WO-US001358.
 31-JAN-2000; 2000US-0179065P.
 04-FEB-2000; 2000US-0180628P.
 24-FEB-2000; 2000US-0184664P.
 02-MAR-2000; 2000US-0186350P.
 16-MAR-2000; 2000US-0189874P.
 17-MAR-2000; 2000US-0190076P.
 18-APR-2000; 2000US-0198123P.
 19-MAY-2000; 2000US-0205515P.
 07-JUN-2000; 2000US-0209467P.
 28-JUN-2000; 2000US-0214886P.
 30-JUN-2000; 2000US-0215135P.
 07-JUL-2000; 2000US-0216647P.
 07-JUL-2000; 2000US-0216880P.
 11-JUL-2000; 2000US-0217487P.
 11-JUL-2000; 2000US-0217496P.
 14-JUL-2000; 2000US-0218290P.
 26-JUL-2000; 2000US-0220963P.
 26-JUL-2000; 2000US-0220964P.
 14-AUG-2000; 2000US-0224518P.
 14-AUG-2000; 2000US-0224519P.
 14-AUG-2000; 2000US-0225213P.
 14-AUG-2000; 2000US-0225214P.
 14-AUG-2000; 2000US-0225266P.
 14-AUG-2000; 2000US-0225267P.
 14-AUG-2000; 2000US-0225268P.
 14-AUG-2000; 2000US-023270P.
 14-AUG-2000; 2000US-0232447P.
 14-AUG-2000; 2000US-0232577P.
 14-AUG-2000; 2000US-0232578P.
 14-AUG-2000; 2000US-0232579P.
 18-AUG-2000; 2000US-0232679P.
 22-AUG-2000; 2000US-0232681P.
 22-AUG-2000; 2000US-0232686P.
 22-AUG-2000; 2000US-02327182P.
 23-AUG-2000; 2000US-0232709P.
 30-AUG-2000; 2000US-0232892P.
 01-SEP-2000; 2000US-0232928P.
 01-SEP-2000; 2000US-0232934P.
 01-SEP-2000; 2000US-0232934P.
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 05-SEP-2000; 2000US-0232934P.
 05-SEP-2000; 2000US-0232934P.
 05-SEP-2000; 2000US-0232934P.
 06-SEP-2000; 2000US-0230437P.
 08-SEP-2000; 2000US-0231242P.
 08-SEP-2000; 2000US-0231243P.
 08-SEP-2000; 2000US-0231244P.
 08-SEP-2000; 2000US-0231413P.
 08-SEP-2000; 2000US-0231414P.
 08-SEP-2000; 2000US-0232080P.
 08-SEP-2000; 2000US-0232081P.
 12-SEP-2000; 2000US-0231968P.
 14-SEP-2000; 2000US-0232397P.
 14-SEP-2000; 2000US-0232398P.
 14-SEP-2000; 2000US-0232399P.
 14-SEP-2000; 2000US-0232400P.
 14-SEP-2000; 2000US-0232401P.
 14-SEP-2000; 2000US-0233063P.
 14-SEP-2000; 2000US-0233064P.
 14-SEP-2000; 2000US-0233065P.
 21-SEP-2000; 2000US-0234223P.
 21-SEP-2000; 2000US-0234274P.
 25-SEP-2000; 2000US-0234957P.
 25-SEP-2000; 2000US-0234958P.
 26-SEP-2000; 2000US-0235484P.
 27-SEP-2000; 2000US-0235834P.
 27-SEP-2000; 2000US-0235836P.

PR	29-SEP-2000;	2000US-0236327P.	XX	WPI; 2001-465558/50.
PR	29-SEP-2000;	2000US-0236367P.	DR	
PR	29-SEP-2000;	2000US-0236368P.	XX	
PR	29-SEP-2000;	2000US-0236369P.	PT	Novel polypeptides and polynucleotides useful as diagnostic reagents to
PR	29-SEP-2000;	2000US-0236370P.	PT	diagnose diseases or disorders associated with aberrant expression or
PR	02-OCT-2000;	2000US-0236802P.	PT	activity of polypeptides, and for treating cancers, rheumatoid arthritis.
PR	02-OCT-2000;	2000US-0237037P.	XX	
PR	02-OCT-2000;	2000US-0237038P.	PS	Disclosure; SEQ ID NO 592; 687pp; English.
PR	02-OCT-2000;	2000US-0237039P.	XX	
PR	02-OCT-2000;	2000US-0237040P.	CC	The present invention relates to the isolation of novel human neoplastic
PR	13-OCT-2000;	2000US-0239335P.	CC	disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA
PR	13-OCT-2000;	2000US-0239937P.	CC	sequences encoding for these polypeptides. The sequences of the invention
PR	20-OCT-2000;	2000US-0240960P.	CC	are useful in the diagnosis, treatment, prevention and/or prognosis of
PR	20-OCT-2000;	2000US-0241121P.	CC	disorders involving neoplastic disease such as hyperproliferative
PR	20-OCT-2000;	2000US-0241785P.	CC	disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem
PR	20-OCT-2000;	2000US-0241786P.	CC	glioma, adult liver cancer, childhood cerebellar astrocytoma, or
PR	20-OCT-2000;	2000US-0241787P.	CC	Hodgkin's lymphoma). The sequences of the invention may also be useful
PR	20-OCT-2000;	2000US-0241808P.	CC	for treating other disorders such as neural disorders, immune system
PR	20-OCT-2000;	2000US-0241809P.	CC	disorders, muscular disorders, reproductive disorders, gastrointestinal
PR	20-OCT-2000;	2000US-0241826P.	CC	disorders, pulmonary disorders, cardiovascular disorders and renal
PR	01-NOV-2000;	2000US-0244617P.	CC	disorders. The polynucleotide sequences of the invention are also useful
PR	08-NOV-2000;	2000US-0246474P.	CC	in gene therapy. AAS35051-AAS35125 represent DNA sequences encoding for
PR	08-NOV-2000;	2000US-0246475P.	CC	the novel human neoplastic disease associated polypeptides of the
PR	08-NOV-2000;	2000US-0246476P.	CC	invention. Note: The sequence data for this patent did not form part of
PR	08-NOV-2000;	2000US-0246477P.	CC	the printed specification, but was obtained in electronic format directly
PR	08-NOV-2000;	2000US-0246478P.	CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
PR	08-NOV-2000;	2000US-0246523P.	XX	
PR	08-NOV-2000;	2000US-0246524P.	SQ	Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;
PR	08-NOV-2000;	2000US-0246525P.		
PR	08-NOV-2000;	2000US-0246526P.		
PR	08-NOV-2000;	2000US-0246527P.		
PR	08-NOV-2000;	2000US-0246528P.		
PR	08-NOV-2000;	2000US-0246532P.		
PR	08-NOV-2000;	2000US-0246609P.		
PR	08-NOV-2000;	2000US-0246610P.		
PR	08-NOV-2000;	2000US-0246611P.		
PR	08-NOV-2000;	2000US-0246613P.		
PR	17-NOV-2000;	2000US-0249207P.		
PR	17-NOV-2000;	2000US-0249208P.		
PR	17-NOV-2000;	2000US-0249209P.		
PR	17-NOV-2000;	2000US-0249210P.		
PR	17-NOV-2000;	2000US-0249211P.		
PR	17-NOV-2000;	2000US-0249212P.		
PR	17-NOV-2000;	2000US-0249213P.		
PR	17-NOV-2000;	2000US-0249214P.		
PR	17-NOV-2000;	2000US-0249215P.		
PR	17-NOV-2000;	2000US-0249216P.		
PR	17-NOV-2000;	2000US-0249217P.		
PR	17-NOV-2000;	2000US-0249218P.		
PR	17-NOV-2000;	2000US-0249244P.		
PR	17-NOV-2000;	2000US-0249245P.		
PR	17-NOV-2000;	2000US-0249264P.		
PR	17-NOV-2000;	2000US-0249265P.		
PR	17-NOV-2000;	2000US-0249279P.		
PR	17-NOV-2000;	2000US-0249299P.		
PR	17-NOV-2000;	2000US-0249300P.		
PR	01-DEC-2000;	2000US-0250160P.		
PR	05-DEC-2000;	2000US-0250391P.		
PR	05-DEC-2000;	2000US-0251030P.		
PR	05-DEC-2000;	2000US-0251988P.		
PR	05-DEC-2000;	2000US-0256719P.		
PR	06-DEC-2000;	2000US-0251475P.		
PR	08-DEC-2000;	2000US-0251868P.		
PR	08-DEC-2000;	2000US-0251869P.		
PR	08-DEC-2000;	2000US-0251989P.		
PR	08-DEC-2000;	2000US-0251990P.		
PR	11-DEC-2000;	2000US-0254097P.		
PR	05-JAN-2001;	2001US-0259678P.		
XX				(HUMA-) HUMAN GENOME SCI INC.
PA				Rosen CA, Barash SC, Ruben SM;
XX				
PI				

QY	1	ATGTGGACAGCTGTGACGCAACTTCTCTGCTGTACCATGAGTCTGTGGGTATCGT	60
DB	637	ATGTGGACAGCTGTGACGCAACTTCTCTGCTGTACCATGAGTCTGTGGGTATCGT	696
QY	61	TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGCAACCGTGGCAATGTGCTC	120
DB	697	TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGCAACCGTGGCAATGTGCTC	756
QY	121	ACCTTACTGGCTTGGGCAATCCAGCCCAAGTCCGTACCGATCAACCTGCTCATAGCC	180
DB	757	ACCTTACTGGCTTGGGCAATCCAGCCCAAGTCCGTACCGATCAACCTGCTCATAGCC	816
QY	181	AACCTCACACTGGGTGATCTCTTACTGCAAGCTCTCTTCTGAGCCCTTCTCTGTGACACC	240
DB	817	AACCTCACACTGGGTGATCTCTTACTGCAAGCTCTCTTCTGAGCCCTTCTCTGTGACACC	876
QY	241	TACCTTCACTGCACTGGGCAACCGGTGCAACCTTCTGCAAGGTATTTGGGCTCTCTT	300
DB	877	TACCTTCACTGCACTGGGCAACCGGTGCAACCTTCTGCAAGGTATTTGGGCTCTCTT	936
QY	301	TTTGCTCCCAATTTCTGCTCCATCTGACCTCTGCTCATGCACTGGGCAACGCTACCTC	360
DB	937	TTTGCTCCCAATTTCTGCTCCATCTGACCTCTGCTCATGCACTGGGCAACGCTACCTC	996
QY	361	CTCATTTGCCCACTTAAGCTTTTCCCAAGTTTTCAGTGTGCAAGGGGATAGTCTGGCA	420
DB	997	CTCATTTGCCCACTTAAGCTTTTCCCAAGTTTTCAGTGTGCAAGGGGATAGTCTGGCA	1056
QY	421	CTGGTGACACCTGGGTTGTGGGGTGGGCACTTCTCCCTCTGCTGCTTATTATATC	480
DB	1057	CTGGTGACACCTGGGTTGTGGGGTGGGCACTTCTCCCTCTGCTGCTTATTATATC	1116
QY	481	CTGGTACCTGTAGTCTGACCTGACCTTTTACCCGATTCGAGCCCGGCTTACACACC	540
DB	1117	CTGGTACCTGTAGTCTGACCTGACCTTTTACCCGATTCGAGCCCGGCTTACACACC	1176
QY	541	ATCCTCATGGGCATCTACTTTTGTCTTGGGCTGACGAGTGTGGCATCTTCTATTGCTC	600
DB	1177	ATCCTCATGGGCATCTACTTTTGTCTTGGGCTGACGAGTGTGGCATCTTCTATTGCTC	1236

Query Match 100.0%; Score 1191; DB 4; Length 2046;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	601	ATCCACCGCCAGGTCAAGAGCAGACACAGGCACTGGACCAATACAAGTTGCGCAGGCA	660	07-JUL-2000;	2000US-0216647P.
Db	1237	ATCCACCGCCAGGTCAAGAGCAGACACAGGCACTGGACCAATACAAGTTGCGCAGGCA	1296	07-JUL-2000;	2000US-0216880P.
QY	661	AGCATCCACTCAACCATGTGCGCCAGGACTGATGAGGCCATCCCTGCTGCTTCCAGGAG	720	11-JUL-2000;	2000US-0217496P.
Db	1297	AGCATCCACTCAACCATGTGCGCCAGGACTGATGAGGCCATCCCTGCTGCTTCCAGGAG	1356	14-JUL-2000;	2000US-0218390P.
QY	721	CTGGACACAGGTTAGCATCAGAGGAGCCCATGAGGGGATTCATCTGAGCCAGTCACT	780	26-JUL-2000;	2000US-0220963P.
Db	1357	CTGGACACAGGTTAGCATCAGAGGAGCCCATGAGGGGATTCATCTGAGCCAGTCACT	1416	14-AUG-2000;	2000US-0220964P.
QY	781	GCTGCCACCAACCCAGACCTCGAAGGGGACTCATCAGAAAGTGGGAGACACAGATCAACAGC	840	14-AUG-2000;	2000US-0224518P.
Db	1417	GCTGCCACCAACCCAGACCTCGAAGGGGACTCATCAGAAAGTGGGAGACACAGATCAACAGC	1476	14-AUG-2000;	2000US-0224519P.
QY	841	AAGAGAGCTAAGCAGATGCGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCCGAGCA	900	14-AUG-2000;	2000US-0225213P.
Db	1477	AAGAGAGCTAAGCAGATGCGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCCGAGCA	1536	14-AUG-2000;	2000US-0225214P.
QY	901	ATTAAGGAGCAGAGAGCTCCGGATCTTCATCGGAATTTGGGAAGTGACTCGAATG	960	14-AUG-2000;	2000US-0225267P.
Db	1537	ATTAAGGAGCAGAGAGCTCCGGATCTTCATCGGAATTTGGGAAGTGACTCGAATG	1596	14-AUG-2000;	2000US-0225268P.
QY	961	TGTTTTGCTGCTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTCTGCTCAACATT	1020	14-AUG-2000;	2000US-0225270P.
Db	1597	TGTTTTGCTGCTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTCTGCTCAACATT	1656	14-AUG-2000;	2000US-0225447P.
QY	1021	CTGGATGCCAGATCCAGCTCCCGGGTGGTCCCATGCTTGTGCCAAGCTCACTCGG	1080	14-AUG-2000;	2000US-0225472P.
Db	1657	CTGGATGCCAGATCCAGCTCCCGGGTGGTCCCATGCTTGTGCCAAGCTCACTCGG	1716	14-AUG-2000;	2000US-0225578P.
QY	1081	CTCAATGTTGATCAACCTGTGCTCTATGAGGATGAAACCGCAATTCGGCCAAAGCA	1140	14-AUG-2000;	2000US-0225579P.
Db	1717	CTCAATGTTGATCAACCTGTGCTCTATGAGGATGAAACCGCAATTCGGCCAAAGCA	1776	18-AUG-2000;	2000US-0226279P.
QY	1141	TATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG	1191	22-AUG-2000;	2000US-0226681P.
Db	1777	TATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG	1827	22-AUG-2000;	2000US-0226688P.
RESULT 13					
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ID	AAK77581	standard; DNA; 2046 BP.			
AC	AAK77581;				
XX					
DT	07-NOV-2001 (first entry)				
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32393.				
XX					
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;				
KW	cytostatic; gene therapy; vaccine; metastasis; ds.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200157182-A2.				
XX					
PD	09-AUG-2001.				
XX					
PF	17-JAN-2001; 2001WO-US001354.				
XX					
PR	31-JAN-2000; 2000US-0179065P.				
PR	04-FEB-2000; 2000US-0180628P.				
PR	24-FEB-2000; 2000US-0184664P.				
PR	02-MAR-2000; 2000US-0186350P.				
PR	16-MAR-2000; 2000US-0189874P.				
PR	17-MAR-2000; 2000US-0190076P.				
PR	18-APR-2000; 2000US-0198123P.				
PR	19-MAY-2000; 2000US-0205151P.				
PR	07-JUN-2000; 2000US-0209467P.				
PR	28-JUN-2000; 2000US-0214886P.				
PR	30-JUN-2000; 2000US-0215135P.				

us-10-029-436-1_copy_61_1251.rng

CC	polynucleotides may be used to produce the secreted (I), by inserting the
CC	nucleic acids into a host cell and culturing the cell to express the
CC	protein. (i) proteins and polynucleotides may be used to prevent,
CC	diagnose and treat immune/haematopoietic-related diseases, especially,
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC	to AAK87694 represent human immune/haematopoietic antigen genomic
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC	represent sequences used in the exemplification of the present invention
XX	
SQ	Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;
Query Match	100.0%; Score 1191; DB 4; Length 2046;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGTGGACAGCTCTGACGCCAACTTCTCCTGCTACCATAGTCTGCTGGGCTATCGT 60
DB	637 ATGTGGACAGCTCTGACGCCAACTTCTCCTGCTACCATAGTCTGCTGGGCTATCGT 696
QY	61 TATGTTGCAGTTAGCTTGGGGGGTGGTGGCTGTGTCAGGCACCGTGGCAATGTGCTC 120
DB	697 TATGTTGCAGTTAGCTTGGGGGGTGGTGGCTGTGTCAGGCACCGTGGCAATGTGCTC 756
QY	131 ACCCTACTGGCCCTTGGGCATTCAGCCCAAGCTCCGTACCCGATTCAACTCTCATAGCC 180
DB	757 ACCCTACTGGCCCTTGGGCATTCAGCCCAAGCTCCGTACCCGATTCAACTCTCATAGCC 816
QY	181 AACCTCACTGGCTGATTCCTCTACTGCAGCTCCTTTCAGCCCTTCTCTGTGGACACC 240
DB	817 AACCTCACTGGCTGATTCCTCTACTGCAGCTCCTTTCAGCCCTTCTCTGTGGACACC 875
QY	241 TACCTCCAACCTGCACTGGGCGCACCGGTGGCACTTCTGCGAGGTAATTGGGCTCTCTGTT 300
DB	877 TACCTCCAACCTGCACTGGGCGCACCGGTGGCACTTCTGCGAGGTAATTGGGCTCTCTGTT 936
QY	301 TTTGGCTCCAAATCTGCTCTCCATCTGACCCCTCTGCTCATCGCATCGGACGCTACCTC 360
DB	937 TTTGGCTCCAAATCTGCTCTCCATCTGACCCCTCTGCTCATCGCATCGGACGCTACCTC 996
QY	361 CTCATTGGCCACCCCTAAGCTTTTTCCTCCCAAGTTTTCAGTGCACAGGGATAGTCTGGCA 420
DB	997 CTCATTGGCCACCCCTAAGCTTTTTCCTCCCAAGTTTTCAGTGCACAGGGATAGTCTGGCA 1056
QY	421 CTGCTGACACCTGGGTTGTGGGCTTGGCCAGCTTGTCTCCCTCTGGCCTATTATTATC 480
DB	1057 CTGCTGACACCTGGGTTGTGGGCTTGGCCAGCTTGTCTCCCTCTGGCCTATTATTATC 1116
QY	481 CTGCTGACCTGTAGTCTGCACCTCTGACCTTTGACCGCATCCGAGGCGGCTTACACCA 540
DB	1117 CTGCTGACCTGTAGTCTGCACCTCTGACCTTTGACCGCATCCGAGGCGGCTTACACCA 1176
QY	541 ATCTCTATPGGCACTCTACTTTGTTGGCTCAGCAGHTTGGCATCTCTTATTTGCTC 600
DB	1177 ATCTCTATPGGCACTCTACTTTGTTGGCTCAGCAGHTTGGCATCTCTTATTTGCTC 1236
QY	601 ATCCACGCCAGGTCAAAACAGACAGACACAGGCACCTGGACCAATACAAGTTGCGACAGGCA 660
DB	1237 ATCCACGCCAGGTCAAAACAGACAGACACAGGCACCTGGACCAATACAAGTTGCGACAGGCA 1296
QY	661 AGCATCCACTCCCAACCATGTGGCCAGGACTGATAGGCCCATGCCCTGTGCTTTCAGGAG 720
DB	1297 AGCATCCACTCCCAACCATGTGGCCAGGACTGATAGGCCCATGCCCTGTGCTTTCAGGAG 1356
QY	721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCAGT 780
DB	1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCAGT 1416
QY	781 GCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAACTGGGAGACAGATCAACAGC 840
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QY	841 AAGAGAGCTAAGCAGATGGCAGAAAGCCCTCCAGAGGATCTGCCAAAGCCCGAGCA 900

Db	1477	AAAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGGCCAGCCA	1536
Qy	901	ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGAAAGGTGACTCGAATG	960
Db	1537	ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGAAAGGTGACTCGAATG	1596
Qy	961	TGTTTTGCTGTGTTCCCTCTGCTTTGCCCTCAGAGTACATCCCTCTTTGCTGCTCAACATT	1020
Db	1597	TGTTTTGCTGTGTTCCCTCTGCTTTGCCCTCAGAGTACATCCCTCTTTGCTGCTCAACATT	1656
Qy	1021	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGTTGCTGCCAACCTCACTCGG	1080
Db	1657	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGTTGCTGCCAACCTCACTCGG	1716
Qy	1081	CTCAATGGTTGCATCAACCCCTGTGCTCTATGCGAGCCATGAACCGCCAAATTCGCCCAAGCA	1140
Db	1717	CTCAATGGTTGCATCAACCCCTGTGCTCTATGCGAGCCATGAACCGCCAAATTCGCCCAAGCA	1776
Qy	1141	TATGGCTCCATTTTAAAGAGAGGCCCGCGAGTTTCCATAGGCTCCATTAG	1191
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RESULT 14

ABA06789
ID ABA06789 standard; DNA; 2046 BP.

AC ABA06789;

10-JAN-2002 (first entry)

Human genomic DNA SEQ ID NO: 875.

Human; gene therapy; neural disorder; immune system disorder;

KW muscular disorder; reproductive disorder; gastrointestinal disorder;

KW pulmonary disorder; cardiovascular disorder; renal disorder;

KW proliferative disorder; inflammation; ds.

OS Homo sapiens.

PN WO200154474-A2.

PD 02-AUG-2001..

17-JAN-2001; 2001WO-US001349.

31-JAN-2000: 2000US-0179065P.

04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

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 08-DEC-2000; 2000US-0251856P.
 08-DEC-2000; 2000US-0251868P.
 08-DEC-2000; 2000US-0251869P.
 08-DEC-2000; 2000US-0251989P.
 08-DEC-2000; 2000US-0251990P.
 11-DEC-2000; 2000US-0254097P.
 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-476161/51.
 Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition.
 Disclosure; SEQ ID NO 875; 859pp + Sequence Listing; English.
 The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a genomic DNA of the invention
 Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1191; DB 4; Length 2046;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 637 ATGTGGAAACAGCTCTGACGCGCAACTTCTCTGTACCATGAGTCTGTGTGGGCTATCGT 696
 61 TATGTTGCAAGTCTGGGGGTGGTGGTGTGTGACAGGACCGCTGGGCAATGTCCTC 120
 697 TATGTTGCAAGTCTGGGGGTGGTGGTGTGTGACAGGACCGCTGGGCAATGTCCTC 756
 121 ACCCTACTGGCTTGGGCAATCCAGCCCAAGCTCCGTACCCGATTCAACCTGTCTATAGCC 180
 757 ACCCTACTGGCTTGGGCAATCCAGCCCAAGCTCCGTACCCGATTCAACCTGTCTATAGCC 816

QY 181 AACCTCACACTGGCTGATCTCTCTACTGACAGCTCTCTCAGCCCTTCTCTGTGGACAC 240
 DB 817 AACCTCACACTGGCTGATCTCTCTACTGACAGCTCTCTCAGCCCTTCTCTGTGGACAC 876
 QY 241 TACCTCCACCTGACCTGGCGCACCGGTGGCCACCTTCTGAGGGATTTGGGCTCTCCCT 300
 DB 877 TACCTCCACCTGACCTGGCGCACCGGTGGCCACCTTCTGAGGGATTTGGGCTCTCCCT 936
 QY 301 TTTGCTCCCAATTTCTGCTCCATCTCTGACCTCTGCTCTCATCGCACTGGGACGCTACCTC 360
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 ID ABK44021 standard; DNA; 2046 BP.
 XX

AC ABK44021;
XX
XX DT
XX 05-JUN-2002 (first entry)
XX Genomic DNA encoding novel central nervous system protein #33.
XX
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
XX WO200155318-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US0011332.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
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PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-581633/65.
 XX
 XX New isolated nucleic acid encoding a protein for diagnosing, preventing,
 PT treating or ameliorating medical conditions and used as food additives or
 PT preservatives.
 PT
 XX Disclosure; SEQ ID NO 1209; 837bp; English.
 PS
 XX The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (III) encoded
 CC by (I), are used to treat a medical condition and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukaemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional

QY 241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTCTGCAAGGGTATTGGGCTCCTCCTT 300
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 DB 1777 TATGCTCCATTTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1827

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2004, 02:47:20 ; Search time 958.703 Seconds
(without alignments)
6292.206 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1191	100.0	1191	13	US-10-343-650A-45
2	1191	100.0	1311	15	Sequence 45, Appli
3	1191	100.0	1438	9	Sequence 1, Appli
4	1191	100.0	1546	15	Sequence 37, Appli
5	1191	100.0	1579	15	Sequence 584, App
6	1191	100.0	1595	15	Sequence 11, Appli
7	1191	100.0	2046	9	Sequence 1, Appli
8	1191	100.0	2046	9	Sequence 875, App
9	1191	100.0	2046	10	Sequence 155, App
10	1191	100.0	2046	10	Sequence 84, Appli
11	1191	100.0	2046	11	Sequence 1209, Ap
12	1191	100.0	2046	13	Sequence 84, Appli
13	1191	100.0	2046	13	Sequence 84, Appli
14	1191	100.0	2046	15	Sequence 130, App
15	1191	100.0	2046	15	Sequence 592, App

15	1188	99.7	1188	15	US-10-094-417-3	Sequence 3, Appli
16	887.6	74.5	1191	15	US-10-094-417-21	Sequence 21, Appli
17	707.6	59.4	1333	15	US-10-017-161-1921	Sequence 1921, Ap
18	475	39.9	525	15	US-10-029-386-12527	Sequence 12527, A
19	357.4	30.0	485	16	US-10-264-237-348	Sequence 348, App
20	345.4	29.0	483	9	US-09-764-853-62	Sequence 62, Appli
21	345.4	29.0	483	10	US-09-389-442-13	Sequence 13, Appli
22	345.4	29.0	483	10	US-09-764-886-26	Sequence 26, Appli
23	345.4	29.0	483	11	US-09-764-875-43	Sequence 43, Appli
24	345.4	29.0	483	13	US-09-764-886-26	Sequence 26, Appli
25	345.4	29.0	483	13	US-09-764-893-14	Sequence 14, Appli
26	345.4	29.0	483	15	US-10-073-865-14	Sequence 14, Appli
27	345.4	29.0	483	15	US-10-103-313-26	Sequence 26, Appli
28	345.4	29.0	483	15	US-10-073-885-38	Sequence 38, Appli
29	209	17.5	209	15	US-10-029-386-26227	Sequence 26227, A
30	133.6	11.2	494	9	US-09-783-590-6339	Sequence 6339, Ap
31	87.8	7.4	1382	15	US-10-225-567A-419	Sequence 419, App
32	87.8	7.4	1382	17	US-10-293-998-4	Sequence 4, Appli
33	87.8	7.4	1584	16	US-10-305-720-284	Sequence 284, App
34	87.8	7.4	1659	13	US-10-391-074-3	Sequence 3, Appli
35	87	7.3	2481	9	US-09-511-822-1	Sequence 1, Appli
36	87	7.3	2481	15	US-10-325-930-1	Sequence 1, Appli
37	86.2	7.2	1663	9	US-09-961-700A-46	Sequence 46, Appli
38	83	7.0	1738	15	US-10-185-991-3	Sequence 3, Appli
39	83	7.0	1738	15	US-10-238-129-3	Sequence 3, Appli
40	83	7.0	1738	15	US-10-238-667-3	Sequence 3, Appli
41	83	7.0	1738	16	US-10-305-720-1402	Sequence 1402, Ap
42	83	7.0	1786	15	US-10-325-567A-35	Sequence 35, Appli
43	80	6.7	1092	15	US-10-303-204A-15	Sequence 15, Appli
44	80	6.7	3129	15	US-10-303-204A-14	Sequence 14, Appli
45	76.6	6.4	2048	14	US-10-052-589-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-343-650A-45
; Sequence 45, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1191)
US-10-343-650A-45

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Best Local Similarity	100.0%;	Pred. No. 0;		
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Gaps	0;			
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Qy	61	TATGTTGAGTTAGTGGGGGGTGGTGGTGGTCTGTGACGACCGTGGGGAATGCTC	120	
Db	61	TATGTTGAGTTAGTGGGGGGTGGTGGTGGTCTGTGACGACCGTGGGGAATGCTC	120	


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; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 584
; LENGTH: 1546
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-584

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TATGTTGAGTACTGGGGGGTGGTGGTGTGTGACAGCACCGTGGGCAATGTGCTC 120
DB 151 TATGTTGAGTACTGGGGGGTGGTGGTGTGTGACAGCACCGTGGGCAATGTGCTC 210
QY 121 ACCCTACTGGCTTGGGCATCCAGCCCAAGCTCGTACCGGATTCAACCTGCTCATAGCC 180
DB 211 ACCCTACTGGCTTGGGCATCCAGCCCAAGCTCGTACCGGATTCAACCTGCTCATAGCC 270
QY 181 AACCTCACTGGTGTATCTCTCTACTGACAGCTCTTTCAGCCCTTCTCTGFGACACC 240
DB 271 AACCTCACTGGTGTATCTCTCTACTGACAGCTCTTTCAGCCCTTCTCTGFGACACC 330
QY 241 TACCTCCACCTGCACTGGCCAGCCGTCACCTCTGACAGGATTTGGGCTCCCTT 300
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DB 391 TTTGCCCTCCAACTTGTCTCCATCTGACCCCTCTGCTCATGCACTGGGACGCTACCTC 450
QY 361 CTCATTGCCACCTAGCTTTTCCCAAGTTTTCAGTCCCAAGGGATAGTGTGGCA 420
DB 451 CTCATTGCCACCTAGCTTTTCCCAAGTTTTCAGTCCCAAGGGATAGTGTGGCA 510
QY 421 CTGCTGAGCACCTGGGTGTGGGGGTGGCCAGCTTTGCTCCCTCTGGCTATTTATATC 480
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DB 1231 TATGCTCTCAATTTAAAGAGGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1281

RESULT 5
US-10-073-885-11
; Sequence 11, Application US/10073885
; Publication No. US20030096346A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ203C1
; CURRENT APPLICATION NUMBER: US/10/073,885
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1554)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-073-885-11

Query Match      100.0%; Score 1191; DB 15; Length 1579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-798-710-1
; Sequence 1, Application US/09798710
; Publication No. US20020187947A1
; GENERAL INFORMATION:
; APPLICANT: Jarai, Gabor
; APPLICANT: Cooper, Paul Roy
; APPLICANT: Yousefi, Shida
; TITLE OF INVENTION: No. US20020187947A1e1 Gene
; FILE REFERENCE: 4-31328A/H026
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; CURRENT APPLICATION NUMBER: US/09/798,710
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/XXX,XXX
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-09-798-710-1
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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 421 CTGTGAGCACCTGGGTTGTGGGCGTGGCAGCTTTGCTCCCTCTGTGGCTATTTATATC 480
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Db 620 CTGTGAGCACCTGGGTTGTGGGCGTGGCAGCTTTGCTCCCTCTGTGGCTATTTATATC 679
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Db 680 ATCTCTCATGGGCTATCTACTTTGTGCTTGGGCTCAGCAGTGTGTCATCTTCTATTTGCTC 739
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Db 740 ATCCACCGCCAGGTCAAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 799
Qy 661 AGCATCCACTCAACCATGTGGCCAGGACTGTGAGGCGATGCTGCTGCTGCTTTCAGGAG 720
Db 800 AGCATCCACTCAACCATGTGGCCAGGACTGTGAGGCGATGCTGCTGCTTTCAGGAG 859
Qy 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCA 780
Db 860 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCA 919
Qy 781 GCTGCCACACCGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCCAGATCAACAGC 840
Db 920 GCTGCCACACCGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCCAGATCAACAGC 979
Qy 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGGATGTGCGCAAGCCCGAGCA 900
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Db 980 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAGCCAGGCCA 1039
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 QY 1021 CTGATGCGCAGAGTCCAGGCTCCCGGGTGTCCACATGTTGCTGCTCAACCTCACTG 1080
 Db 1160 CTGATGCGCAGAGTCCAGGCTCCCGGGTGTCCACATGTTGCTGCTCAACCTCACTG 1219
 QY 1081 CTCATGTTGTCATCAACCTCTGCTCTATGAGCCATGAACGCCAATTCGCCCAAGCA 1140
 Db 1220 CTCATGTTGTCATCAACCTCTGCTCTATGAGCCATGAACGCCAATTCGCCCAAGCA 1279
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 Db 1280 TATGCTCTCAATTTTAAAGAGGCCCCCGGAGTTTCCATAGGCTCCATTAG 1330

RESULT 7

US-09-764-853-875
 ; Sequence 875, Application US/09764853
 ; Patent No. US20020090672A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P0206
 ; CURRENT APPLICATION NUMBER: US/09/764,853
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 939
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 875
 ; LENGTH: 2046
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-853-875

Query Match 100.0%; Score 1191; DB 9; Length 2046;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGGAACAGCTCTGACGCCAATTTCTCTGTACCATGAGTCTGTGCTGGGCTATCGT 60
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 QY 61 TATGTTCCAGTATGCTGGGGGTGGTGGTGTGACAGGACCGTGGCAATGCTC 120
 Db 697 TATGTTCCAGTATGCTGGGGGTGGTGGTGTGACAGGACCGTGGCAATGCTC 756
 QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGCTCATAGCC 180
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 QY 181 AACCTCAGTGGTGTATCTCTCTACTGACGCTCTTCCAGCCCTTCTCTGTGGACACC 240
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 QY 241 TACCTCAGTGGTGTATCTCTCTACTGACGCTCTTCCAGCCCTTCTCTGTGGTCTCTCT 300
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 QY 301 TTGCTCTCAATTTCTGCTCTCACTGACCCCTCTGCTCTATGCACTGGGAGCCTACCTC 360
 Db 937 TTGCTCTCAATTTCTGCTCTCACTGACCCCTCTGCTCTATGCACTGGGAGCCTACCTC 996
 QY 361 CTGATTCGCCACCTAGCTTTTCCCAAGTTTTCAGTCCCAAGGGATAGTGTGGCA 420

Db 997 CTCATTGCCACCCTAAGCTTTTCCCACAGTTTTCAGTGCACAGGGATAGTGTGGCA 1056
 QY 421 CTGGTGAGACCTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGCTCCCTATTATTATC 480
 Db 1057 CTGGTGAGACCTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGCTCCCTATTATTATC 1116
 QY 481 CTGGTACCTGTAGTCTGACCTGACGCTTTTGACCGCATCCGAGCCCGGCTTTACACACC 540
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 QY 541 ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
 Db 1177 ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
 QY 601 ATCCACCCCGCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGCA 660
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 QY 721 CTGGACAGCAGTTAGCATCAGGAGGACCCAGTCAGGGGATTTTCATCTGAGCCAGTCACT 780
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 Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCAAGCCAGCCAGCA 1536
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 Db 1717 CTCATGTTGCTATCAACCTGTGCTCTATGAGCCATGAACCGCCAAATTCGGCCAGCA 1776
 QY 1141 TATGCTCTCAATTTTAAAGAGGCCCCCGGAGTTTCCATAGGCTCCATTAG 1191
 Db 1777 TATGCTCTCAATTTTAAAGAGGCCCCCGGAGTTTCCATAGGCTCCATTAG 1827

RESULT 8

US-09-989-442-155
 ; Sequence 155, Application US/09989442
 ; Publication No. US20030013649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P0208
 ; CURRENT APPLICATION NUMBER: US/09/989,442
 ; CURRENT FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 60/179,065
 ; PRIOR FILING DATE: 2000-01-31
 ; PRIOR APPLICATION NUMBER: 60/180,628
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: 60/214,886
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/217,487
 ; PRIOR FILING DATE: 2000-07-11

1	PRIOR APPLICATION NUMBER: 60/225,755	2
2	PRIOR FILING DATE: 2000-08-14	3
3	PRIOR APPLICATION NUMBER: 60/220,963	4
4	PRIOR FILING DATE: 2000-07-26	5
5	PRIOR APPLICATION NUMBER: 60/217,496	6
6	PRIOR FILING DATE: 2000-07-11	7
7	PRIOR APPLICATION NUMBER: 60/225,447	8
8	PRIOR FILING DATE: 2000-08-14	9
9	PRIOR APPLICATION NUMBER: 60/218,290	10
10	PRIOR FILING DATE: 2000-07-14	11
11	PRIOR APPLICATION NUMBER: 60/225,757	12
12	PRIOR FILING DATE: 2000-08-14	13
13	PRIOR APPLICATION NUMBER: 60/226,868	14
14	PRIOR FILING DATE: 2000-08-22	15
15	PRIOR APPLICATION NUMBER: 60/216,647	16
16	PRIOR FILING DATE: 2000-07-07	17
17	PRIOR APPLICATION NUMBER: 60/225,267	18
18	PRIOR FILING DATE: 2000-08-14	19
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20	PRIOR FILING DATE: 2000-07-07	21
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24	PRIOR FILING DATE: 2000-12-08	25
25	PRIOR APPLICATION NUMBER: 60/235,834	26
26	PRIOR FILING DATE: 2000-09-27	27
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29	PRIOR APPLICATION NUMBER: 60/234,223	30
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31	PRIOR APPLICATION NUMBER: 60/228,924	32
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33	PRIOR APPLICATION NUMBER: 60/224,518	34
34	PRIOR FILING DATE: 2000-08-14	35
35	PRIOR APPLICATION NUMBER: 60/236,369	36
36	PRIOR FILING DATE: 2000-09-29	37
37	PRIOR APPLICATION NUMBER: 60/224,519	38
38	PRIOR FILING DATE: 2000-08-14	39
39	PRIOR APPLICATION NUMBER: 60/220,964	40
40	PRIOR FILING DATE: 2000-07-26	41
41	PRIOR APPLICATION NUMBER: 60/241,809	42
42	PRIOR FILING DATE: 2000-10-20	43
43	PRIOR APPLICATION NUMBER: 60/249,299	44
44	PRIOR FILING DATE: 2000-11-17	45
45	PRIOR APPLICATION NUMBER: 60/236,327	46
46	PRIOR FILING DATE: 2000-09-29	47
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50	PRIOR FILING DATE: 2000-11-01	51
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64	PRIOR FILING DATE: 2000-09-05	65
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66	PRIOR FILING DATE: 2000-09-08	67
67	PRIOR APPLICATION NUMBER: 60/229,509	68

1	PRIOR FILING DATE: 2000-09-05	
2	PRIOR APPLICATION NUMBER: 60/236,367	
3	PRIOR FILING DATE: 2000-09-29	
4	PRIOR APPLICATION NUMBER: 60/237,039	
5	PRIOR FILING DATE: 2000-10-02	
6	PRIOR APPLICATION NUMBER: 60/237,038	
7	PRIOR FILING DATE: 2000-10-02	
8	PRIOR APPLICATION NUMBER: 60/236,370	
9	PRIOR FILING DATE: 2000-09-29	
10	PRIOR APPLICATION NUMBER: 60/236,802	
11	PRIOR FILING DATE: 2000-10-02	
12	PRIOR APPLICATION NUMBER: 60/237,037	
13	PRIOR FILING DATE: 2000-10-02	
14	PRIOR APPLICATION NUMBER: 60/237,040	
15	PRIOR FILING DATE: 2000-10-02	
16	PRIOR APPLICATION NUMBER: 60/240,960	
17	PRIOR FILING DATE: 2000-10-20	
18	PRIOR APPLICATION NUMBER: 60/239,935	
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20	PRIOR APPLICATION NUMBER: 60/239,937	
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26	PRIOR APPLICATION NUMBER: 60/246,532	
27	PRIOR FILING DATE: 2000-11-08	
28	PRIOR APPLICATION NUMBER: 60/249,216	
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34	PRIOR APPLICATION NUMBER: 60/225,759	
35	PRIOR FILING DATE: 2000-08-14	
36	PRIOR APPLICATION NUMBER: 60/225,213	
37	PRIOR FILING DATE: 2000-08-14	
38	PRIOR APPLICATION NUMBER: 60/227,182	
39	PRIOR FILING DATE: 2000-08-22	
40	PRIOR APPLICATION NUMBER: 60/225,214	
41	PRIOR FILING DATE: 2000-08-14	
42	PRIOR APPLICATION NUMBER: 60/235,836	
43	PRIOR FILING DATE: 2000-09-27	
44	PRIOR APPLICATION NUMBER: 60/230,438	
45	PRIOR FILING DATE: 2000-09-06	
46	PRIOR APPLICATION NUMBER: 60/215,135	
47	PRIOR FILING DATE: 2000-06-30	
48	PRIOR APPLICATION NUMBER: 60/225,266	
49	PRIOR FILING DATE: 2000-08-14	
50	PRIOR APPLICATION NUMBER: 60/249,218	
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54	PRIOR APPLICATION NUMBER: 60/249,213	
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56	PRIOR APPLICATION NUMBER: 60/249,212	
57	PRIOR FILING DATE: 2000-11-17	
58	PRIOR APPLICATION NUMBER: 60/249,207	
59	PRIOR FILING DATE: 2000-11-17	
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62	PRIOR APPLICATION NUMBER: 60/249,244	
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66	PRIOR APPLICATION NUMBER: 60/249,211	
67	PRIOR FILING DATE: 2000-11-17	
68	PRIOR APPLICATION NUMBER: 60/249,215	
69	PRIOR FILING DATE: 2000-11-17	
70	PRIOR APPLICATION NUMBER: 60/249,264	
71	PRIOR FILING DATE: 2000-11-17	
72	PRIOR APPLICATION NUMBER: 60/249,214	
73	PRIOR FILING DATE: 2000-11-17	

PRIOR APPLICATION NUMBER: 60/249,297
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/232,400
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/231,242
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 PRIOR APPLICATION NUMBER: 60/241,826
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 PRIOR APPLICATION NUMBER: 60/246,475
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 60/231,243
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/233,065
 PRIOR FILING DATE: 2000-09-14

Query Match 100.0%; Score 1191; DB 10; Length 2046;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGTGGACAGCTGTGACGCGCACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
 637 ATGTGGACAGCTGTGACGCGCACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 696
 61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC 120
 697 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGTGACAGGACCGTGGGCAATGTGCTC 756
 121 ACCCTACTGCTGGCTGCGCATCCAGCCCAAGCTCCGTTACCCGATTCACCTGCTCATAGCC 180
 757 ACCCTACTGCTGGCTGCGCATCCAGCCCAAGCTCCGTTACCCGATTCACCTGCTCATAGCC 816
 181 AACCTCAGCTGCTGCTGCTCTCTACTGACGCTCTCTCTGACGCTCTCTCTGCTGGACCC 240
 817 AACCTCAGCTGCTGCTGCTCTCTACTGACGCTCTCTCTGACGCTCTCTCTGCTGGACCC 876
 241 TACCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 877 TACCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 936
 301 TTTCCCTCCAAATTCGTCTCATCTCTGACCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 360
 937 TTTCCCTCCAAATTCGTCTCATCTCTGACCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 996
 361 CTGATTCGCACTTAAAGCTTTTCCCAAGTTTCCCAAGTTTCCCAAGTTTCCCAAGTTTCCCA 420
 997 CTGATTCGCACTTAAAGCTTTTCCCAAGTTTCCCAAGTTTCCCAAGTTTCCCAAGTTTCCCA 1056
 421 CTGATTCGCACTTAAAGCTTTTCCCAAGTTTCCCAAGTTTCCCAAGTTTCCCAAGTTTCCCA 1480

Db 1057 CTGTTGAGCACCCTGGGTTGTGGGCTGTGGCCAGCTTTGCTCCCTCTGCTCTATTTATATC 1116
 Qy 481 CTGTTGAGCACCCTGGGTTGTGGGCTGTGGCCAGCTTTGCTCCCTCTGCTCTATTTATATC 540
 Db 1117 CTGTTGAGCACCCTGGGTTGTGGGCTGTGGCCAGCTTTGCTCCCTCTGCTCTATTTATATC 1176
 Qy 541 ATCTCTATGGGCATCTACTTTGCTGCTGGGCTGACGAGTGTGGCATCTTCTATTGCTCTC 600
 Db 1177 ATCTCTATGGGCATCTACTTTGCTGCTGGGCTGACGAGTGTGGCATCTTCTATTGCTCTC 1236
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 Db 1237 ATCCACCGCCAGGTCACACGAGCAGCAGCAGCTGACCAATACAAATGTCGACAGGCA 1296
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 Db 1477 AAGAGAGCTAAGCAGATGGCAG 1536
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 Db 1777 TATGCTCCATTTTAAAG 1827

RESULT 9
 US-09-764-886-84/C
 ; Sequence 84, Application US/09764886
 ; Publication No. US2003013927A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT202
 ; CURRENT APPLICATION NUMBER: US/09/764,886
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 84
 ; LENGTH: 2046
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-886-84
 Query Match 100.0%; Score 1191; DB 10; Length 2046;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACCCCACTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 60
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 Db 1290 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCGGATTCGAACCTGCTCATGCC 1231
 QY 181 AACCTCACACTGGCTGATCTCTCTACTGCAAGGCTCTCTTACGCGCTTCTCTGTGACACC 240
 Db 1230 AACCTCACACTGGCTGATCTCTCTACTGCAAGGCTCTCTTACGCGCTTCTCTGTGACACC 1171
 QY 241 TACCTCCACTGACCTGGGCGACCGGTGGCACTTCTGCAAGGATTTGGGCTCTCTCTT 300
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 QY 601 ATCCACCGCAGCTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660
 Db 810 ATCCACCGCAGCTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 751
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 QY 781 GCTGCCACCCAGACCCCTGGAGGGGACTCATCAGAAAGTGGGAGCAGATCAACAGC 840
 Db 630 GCTGCCACCCAGACCCCTGGAGGGGACTCATCAGAAAGTGGGAGCAGATCAACAGC 571
 QY 841 AAGAGAGCTAAGCAGATGGCAGGAAAGCCCTCCAGAGCAGCTCCCAAGGCCAGGCA 900
 Db 570 AAGAGAGCTAAGCAGATGGCAGGAAAGCCCTCCAGAGCAGCTCCCAAGGCCAGGCA 511
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 QY 961 TGTTTTGCTGTGTTCTCTGCTTTGGCTGAGTACATCCCTTCTTGTGCTCAACATT 1020
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 QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTCTGCCAACCTCACTGG 1080
 Db 390 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTCTGCCAACCTCACTGG 331

QY 1081 CTCAATGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACGCCAATTCGCCCAAGCA 1140
 Db 330 CTCAATGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACGCCAATTCGCCCAAGCA 271
 QY 1141 TATGGCTCCATTTTAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
 Db 270 TATGGCTCCATTTTAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 220

RESULT 10
 US-09-764-875-1209
 ; Sequence 1209, Application US/09764875
 ; Publication No. US20040018969A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: RIZ02
 ; CURRENT APPLICATION NUMBER: US/09/764,875
 ; PENDING FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1249
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1209
 ; LENGTH: 2046
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-875-1209

Query Match 100.0%; Score 1191; DB 11; Length 2046;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACCCCACTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 60
 Db 637 ATGTGGAACAGCTCTGACCCCACTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 696
 QY 61 TATGTTGCAAGTTAGCTGGGGGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 120
 Db 697 TATGTTGCAAGTTAGCTGGGGGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 756
 QY 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCGGATTCGAACCTGCTCATGCC 180
 Db 757 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCGGATTCGAACCTGCTCATGCC 816
 QY 181 AACCTCACACTGGCTGATCTCTCTACTGCAAGGCTCTCTTACGCGCTTCTCTGTGACACC 240
 Db 817 AACCTCACACTGGCTGATCTCTCTACTGCAAGGCTCTCTTACGCGCTTCTCTGTGACACC 876
 QY 241 TACCTCCACTGCACTGGGCGACCGGTGGCACTTCTGCAAGGATTTGGGCTCTCTCTT 300
 Db 877 TACCTCCACTGCACTGGGCGACCGGTGGCACTTCTGCAAGGATTTGGGCTCTCTCTT 936
 QY 301 TTTGCTCTCAATTTCTGCTCTCATGCTGACCTCTGCTCTCATGCGACTGGGAGCTACCTC 360
 Db 937 TTTGCTCTCAATTTCTGCTCTCATGCTGACCTCTGCTCTCATGCGACTGGGAGCTACCTC 996
 QY 361 CTCAATGGCCACCTTAAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATGAGTCTGGCA 420
 Db 997 CTCAATGGCCACCTTAAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATGAGTCTGGCA 1056
 QY 421 CTGTTGAGCAGCTGGGTGGGGTGGGCGTGGGCGATTTGCTCCCTCTGCGCTATTTATATC 480
 Db 1057 CTGTTGAGCAGCTGGGTGGGGTGGGCGTGGGCGATTTGCTCCCTCTGCGCTATTTATATC 1116
 QY 481 CTGGTACTGCTAGTCTGCACTGCGAGCTTTGACCGCATCCGAGCGCGGCTTACACCACC 540
 Db 1117 CTGGTACTGCTAGTCTGCACTGCGAGCTTTGACCGCATCCGAGCGCGGCTTACACCACC 1176
 QY 541 ATCCTCATGGGCACTACTTTTGTGCTTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
 Db 1177 ATCCTCATGGGCACTACTTTTGTGCTTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
 QY 601 ATCCACCGCAGCTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660

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Db 1237 ATCCACGCCAGGTCACCAACGAGCAGCAGGCACTGGACCAATACAAAGTTGGACAGGCA 1296
Qy 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGTGCTGTTTCCAGGAG 720
Db 1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGTGCTGTTTCCAGGAG 1356
Qy 721 CTGACAGCAGGTTAGCATCAGAGGAGCCAGTGGAGGGATTTCACTGAGCCAGTCAAGT 780
Db 1357 CTGACAGCAGGTTAGCATCAGAGGAGCCAGTGGAGGGATTTCACTGAGCCAGTCAAGT 1416
Qy 781 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGAGACCAAGTCAACAGC 840
Db 1417 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGAGACCAAGTCAACAGC 1476
Qy 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCTAAAGCCCAAGCCA 900
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCTAAAGCCCAAGCCA 1536
Qy 901 ATTAAGGAGCCAGAGAGCTCCGATTTCTTCATCGGAATTTGGAGGAGTCAATCGAATG 960
Db 1537 ATTAAGGAGCCAGAGAGCTCCGATTTCTTCATCGGAATTTGGAGGAGTCAATCGAATG 1596
Qy 961 TGTGTTGCTGTGTTTCTGCTGTTTGGCCCTGAGCTACATCCCTTTCTGCTGCTCAACAT 1020
Db 1597 TGTGTTGCTGTGTTTCTGCTGTTTGGCCCTGAGCTACATCCCTTTCTGCTGCTCAACAT 1656
Qy 1021 CTGATGCCAGAGTCCAGGCTCCCGGGGTGTCACATGCTTGTGCTGCAACCTCACTG 1080
Db 1657 CTGATGCCAGAGTCCAGGCTCCCGGGGTGTCACATGCTTGTGCTGCAACCTCACTG 1716
Qy 1081 CTCAATGGTTCATCAACCCCTGCTCTATGACAGCCATGAACGCCAATTCGCCCAAGCA 1140
Db 1717 CTCAATGGTTCATCAACCCCTGCTCTATGACAGCCATGAACGCCAATTCGCCCAAGCA 1776
Qy 1141 TATGGCTCCATTTAAAGAGGCCCCGAGTTTCCATAGGCTCCATTTAG 1191
Db 1777 TATGGCTCCATTTAAAGAGGCCCCGAGTTTCCATAGGCTCCATTTAG 1827

RESULT 11
US-09-764-886-84/c
; Sequence 84, Application US/09764886
; Publication No. US20020086822A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-886-84

Query Match 100.0%; Score 1191; DB 13; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGAACAGCTCTGACGCACTTCTCTGCTACCATGATGCTGTGGCTATCGT 60
Db 1410 ATGTGGAACAGCTCTGACGCACTTCTCTGCTACCATGATGCTGTGGCTATCGT 1351
Qy 61 TATGTTTCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCCGTGGGCAATGTGCTC 120
Db 1350 TATGTTTCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCCGTGGGCAATGTGCTC 1291
Qy 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGTCTATAGCC 180
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RESULT 12

US-09-764-893-130

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Qy 181 AACCTCACACTGGCTGATCTCTCTACTGACGCTCTCTTACGCCCTTCTCTGTGGACACC 240
Db 1230 AACCTCACACTGGCTGATCTCTCTACTGACGCTCTCTTACGCCCTTCTCTGTGGACACC 1171
Qy 241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAAGGATTTGGGCTCTCTCTT 300
Db 1170 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAAGGATTTGGGCTCTCTCTT 1111
Qy 301 TTTGGCTCCAAATTTCTGCTCCATCTGACCCCTTGCCTCATCGCACTGGGACGTCATCTC 360
Db 1110 TTTGGCTCCAAATTTCTGCTCCATCTGACCCCTTGCCTCATCGCACTGGGACGTCATCTC 1051
Qy 361 CTCAATGGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCAGAGGATAGTCTGGCA 420
Db 1050 CTCAATGGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCAGAGGATAGTCTGGCA 991
Qy 421 CTGCTGACCACTGGGTTGTGGGCTGCGCCAGCTTTGCTCCCTCTGCTCTATTTATATC 480
Db 990 CTGCTGACCACTGGGTTGTGGGCTGCGCCAGCTTTGCTCCCTCTGCTCTATTTATATC 931
Qy 481 CTGCTGACCACTGGGTTGTGGGCTGCGCCAGCTTTGCTCCCTCTGCTCTATTTATATC 540
Db 930 CTGCTGACCACTGGGTTGTGGGCTGCGCCAGCTTTGCTCCCTCTGCTCTATTTATATC 871
Qy 541 ATCTCTATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db 870 ATCTCTATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 811
Qy 601 ATCCACCCCAAGGTCACACGAGCAGCAGCACTGACCAATCAAGTTGCGCAGGCA 660
Db 810 ATCCACCCCAAGGTCACACGAGCAGCAGCACTGACCAATCAAGTTGCGCAGGCA 751
Qy 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGTGCTTCCAGGAG 720
Db 750 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGTGCTTCCAGGAG 691
Qy 721 CTGGAACAGCAGGTTAGCATCAGGAGGACCCAGTGGAGGGATTTTCATCTGAGCCAGTCA 780
Db 690 CTGGAACAGCAGGTTAGCATCAGGAGGACCCAGTGGAGGGATTTTCATCTGAGCCAGTCA 631
Qy 781 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCATCAACAGC 840
Db 630 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCATCAACAGC 571
Qy 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCCAAGCCA 900
Db 570 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCCAAGCCA 511
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Qy 961 TGTGTTGCTGTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
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Db 390 CTGATGCCAGAGTCCAGGCTCCCGGGGTGTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 331
Qy 1081 CTCAATGGTTCATCAACCCCTGCTCTATGACGCCATGAACGCCCAATTCGCGCAAGCA 1140
Db 330 CTCAATGGTTCATCAACCCCTGCTCTATGACGCCATGAACGCCCAATTCGCGCAAGCA 271
Qy 1141 TATGGCTCCATTTTAAAGAGGCCCCGAGTTTCCATAGGCTCCATTTAG 1191
Db 270 TATGGCTCCATTTTAAAGAGGCCCCGAGTTTCCATAGGCTCCATTTAG 220
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; Sequence 130, Application US/09764893
; Publication No. US20020086330A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P209
; CURRENT APPLICATION NUMBER: US/09/764,893
; CURRENT FILING DATE: 2001-01-19
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 130
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-893-130

Query Match 100.0%; Score 1191; DB 13; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAATCTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT 60
Db 637 ATGTGGAACAGCTCTGACGCCAATCTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT 696
QY 61 TATGTTGCAAGTGTAGCTGGGGGTGGTGGTGTGTCACAGCAGCAGTGGGCAATGTGTC 120
Db 697 TATGTTGCAAGTGTAGCTGGGGGTGGTGGTGTGTCACAGCAGCAGTGGGCAATGTGTC 756
QY 121 ACCCTACTGGCCCTGACCTGACCCCAAGCTCCGTACCCGATTCACCGTGTCTATAGCC 180
Db 757 ACCCTACTGGCCCTGACCCCAAGCTCCGTACCCGATTCACCGTGTCTATAGCC 816
QY 181 AACCTCAGCTGGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 817 AACCTCAGCTGGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 296
QY 241 TATGTTGCAAGTGTAGCTGGGGGTGGTGGTGTGTCACAGCAGCAGTGGGCAATGTGTC 300
Db 877 TATGTTGCAAGTGTAGCTGGGGGTGGTGGTGTGTCACAGCAGCAGTGGGCAATGTGTC 936
QY 301 TTTGGCTCCAAATCTGCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 937 TTTGGCTCCAAATCTGCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
QY 361 CTCATTGCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 420
Db 997 CTCATTGCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 1056
QY 421 CTGGTGAGCAGCTGGGTGTGGGCGTGGGCGAGCTTTGCTCCCTCTGCGCTATTTATATC 480
Db 1057 CTGGTGAGCAGCTGGGTGTGGGCGTGGGCGAGCTTTGCTCCCTCTGCGCTATTTATATC 1116
QY 481 CTGGTACCTGTAGCTGCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 540
Db 1117 CTGGTACCTGTAGCTGCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 1176
QY 541 ATCCTCATGGGCTATCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 1177 ATCCTCATGGGCTATCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1236
QY 601 ATCCAGCGCCAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660
Db 1237 ATCCAGCGCCAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1296
QY 661 AGCATCCACTCCAAACATGTGGCCAGGCTGATGAGGCCATGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 1297 AGCATCCACTCCAAACATGTGGCCAGGCTGATGAGGCCATGCTGCTGCTGCTGCTGCTGCTGCT 1356
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGAGGATTTTCATCTGAGCCAGTCACT 780
Db 1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGAGGATTTTCATCTGAGCCAGTCACT 1416

QY 781 GCTGCCACCAACCCAGAGCTGGAGGGAGTCTATCAGAGTGGGAGCACCAGATCAACAGC 840
Db 1417 GCTGCCACCAACCCAGAGCTGGAGGGAGTCTATCAGAGTGGGAGCACCAGATCAACAGC 1476
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 900
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 1536
QY 901 ATTAAGAGCAGCAGAGAGCTCCGGATCTTTCATCGGAATTTGGGAAGTGTGCTGCAATG 960
Db 1537 ATTAAGAGCAGCAGAGAGCTCCGGATCTTTCATCGGAATTTGGGAAGTGTGCTGCAATG 1596
QY 961 TGTGTTGCTGTGTTCTCTGCTTTCCTGCTGAGTGTATCCCTTCTTCTGCTGCTCAACATT 1020
Db 1597 TGTGTTGCTGTGTTCTCTGCTTTCCTGCTGAGTGTATCCCTTCTTCTGCTGCTCAACATT 1656
QY 1021 CTGATGCCAGAGTCCAGGCTCCCGGGTGTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1657 CTGATGCCAGAGTCCAGGCTCCCGGGTGTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1716
QY 1081 CTCATGTTGCTATCAACCTGTGCTCTATGACGCAATGAACGCCAATTCGGCCAAAGCA 1140
Db 1717 CTCATGTTGCTATCAACCTGTGCTCTATGACGCAATGAACGCCAATTCGGCCAAAGCA 1776
QY 1141 TATGGCTCCATTTTAAAGAGGCGCCCGAGTTCCTATAGGCTCCATTAG 1191
Db 1777 TATGGCTCCATTTTAAAGAGGCGCCCGAGTTCCTATAGGCTCCATTAG 1827

RESULT 13
US-10-073-865-130
; Sequence 130, Application US/10073865
; Publication No. US20030044904A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P209C1
; CURRENT APPLICATION NUMBER: US/10/073,865
; CURRENT FILING DATE: 2002-02-14
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 130
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-073-865-130

Query Match 100.0%; Score 1191; DB 15; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAATCTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT 60
Db 637 ATGTGGAACAGCTCTGACGCCAATCTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT 696
QY 61 TATGTTGCAAGTGTAGCTGGGGGTGGTGGTGTGTCACAGCAGCAGTGGGCAATGTGTC 120
Db 697 TATGTTGCAAGTGTAGCTGGGGGTGGTGGTGTGTCACAGCAGCAGTGGGCAATGTGTC 756
QY 121 ACCCTACTGGCCCTGACCTGACCCCAAGCTCCGTACCCGATTCACCGTGTCTATAGCC 180
Db 757 ACCCTACTGGCCCTGACCCCAAGCTCCGTACCCGATTCACCGTGTCTATAGCC 816
QY 181 AACCTCAGCTGGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 817 AACCTCAGCTGGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 296
QY 241 TATGTTGCAAGTGTAGCTGGGGGTGGTGGTGTGTCACAGCAGCAGTGGGCAATGTGTC 300
Db 877 TATGTTGCAAGTGTAGCTGGGGGTGGTGGTGTGTCACAGCAGCAGTGGGCAATGTGTC 936
QY 301 TTTGGCTCCAAATCTGCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 961 TGTGTTGCTGTGTTCTCTGCTTTGGCTGAGCTACATCCCTTCTGCTGCTCAACATT 1020
Db 1597 TGTGTTGCTGTGTTCTCTGCTTTGGCTGAGCTACATCCCTTCTGCTGCTCAACATT 1656
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACCCTGG 1080
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACCCTGG 1716
QY 1081 CTCATGTTGATCAACCTGTGCTCTATGAGGCAATGAACCGCAATTCGCGCAAGCA 1140
Db 1717 CTCATGTTGATCAACCTGTGCTCTATGAGGCAATGAACCGCAATTCGCGCAAGCA 1776
QY 1141 TATGGCTCCATTTTAAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1777 TATGGCTCCATTTTAAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1827

RESULT 15

US-10-094-417-3
; Sequence 3, Application US/10094417
; Publication No. US20030045685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030045685A1e1 Receptors
; FILE REFERENCE: 018781-008110US
; CURRENT APPLICATION NUMBER: US/10/094,417
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/802,803
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/276,649
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1188)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
US-10-094-417-3

Query Match 99.7%; Score 1188; DB 15; Length 1188;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGAAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 60
Db 1 ATGTGAAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 60
QY 61 TATGTTGCACTAGCTGGGGGTGGTGGTGTGACAGGCAACCGTGGGCAATGCTC 120
Db 61 TATGTTGCACTAGCTGGGGGTGGTGGTGTGACAGGCAACCGTGGGCAATGCTC 120
QY 121 ACCCTACTGGCCCTGGCCATCCAGCCCAAGCTCCGTACCCGATTAACCTGCTCATAGCC 180
Db 121 ACCCTACTGGCCCTGGCCATCCAGCCCAAGCTCCGTACCCGATTAACCTGCTCATAGCC 180
QY 181 AACCTACACTGGCTGATCTCTACTGACAGCTCTTTCAGCCCTTCTCTGTTGGACACC 240
Db 181 AACCTACACTGGCTGATCTCTACTGACAGCTCTTTCAGCCCTTCTCTGTTGGACACC 240
QY 241 TACCTCACCTGCACTGGCGCAACCGGTGCCACCTTCTGCAAGGTAATTGGGGTCTCTCTT 300
Db 241 TACCTCACCTGCACTGGCGCAACCGGTGCCACCTTCTGCAAGGTAATTGGGGTCTCTCTT 300

Search completed: September 24, 2004, 08:34:15
Job time : 961.703 secs

QY 301 TTTGCTCCCAATTTCTCTCCATCTGCTGACCCCTGTGCTCATGCACTGGGACGCTACCTC 360
Db 301 TTTGCTCCCAATTTCTCTCTCATCTGACCCCTGTGCTCATGCACTGGGACGCTACCTC 360
QY 361 CTCATTTGCCACACCTTAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGCGCA 420
Db 361 CTCATTTGCCACACCTTAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGCGCA 420
QY 421 CTGCTGAGCACTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGGCTATTTATATC 480
Db 421 CTGCTGAGCACTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGGCTATTTATATC 480
QY 481 CTGCTACTGTAGTCTGACCTGAGCTTGAACGCAATCCGAGCCGCGCTTACACCAACC 540
Db 481 CTGCTACTGTAGTCTGACCTGAGCTTGAACGCAATCCGAGCCGCGCTTACACCAACC 540
QY 541 ATCCTCATGGGCATCTACTTTGTGCTTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db 541 ATCCTCATGGGCATCTACTTTGTGCTTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
QY 601 ATCCACCGCAGGTTCAACGAGCAGCAGGCTTGGACCAATACAAGTTGCGACAGGCA 660
Db 601 ATCCACCGCAGGTTCAACGAGCAGCAGGCTTGGACCAATACAAGTTGCGACAGGCA 660
QY 661 AGCATCCACTCCAACTGTGGCCAGGCTGATGAGGCCATGCTGCTGCTTCCAGGAG 720
Db 661 AGCATCCACTCCAACTGTGGCCAGGCTGATGAGGCCATGCTGCTGCTTCCAGGAG 720
QY 721 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCA 780
Db 721 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCA 780
QY 781 GCTGCCACCCAGACCCCTGGAGGGGACTCATCAGAAGTGGGAGACCATCAACAGC 840
Db 781 GCTGCCACCCAGACCCCTGGAGGGGACTCATCAGAAGTGGGAGACCATCAACAGC 840
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
Db 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
QY 901 ATTAAGAGCCAGAGCTCCCGGATTTTCATCGGAATTTGGAGAGTGAATCGAATG 960
Db 901 ATTAAGAGCCAGAGAGCTCCCGGATTTTCATCGGAATTTGGAGAGTGAATCGAATG 960
QY 961 TGTGTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 961 TGTGTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
QY 1021 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCCATGCTTGTGCTGCAACCTCACCCTGG 1080
Db 1021 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCCATGCTTGTGCTGCAACCTCACCCTGG 1080
QY 1081 CTCATGTTGTCATCAACCTTGTGCTTATGAGCCATGAACCGCAATTCGCGCAAGCA 1140
Db 1081 CTCATGTTGTCATCAACCTTGTGCTTATGAGCCATGAACCGCAATTCGCGCAAGCA 1140
QY 1141 TATGGCTCCATTTTAAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCAT 1188
Db 1141 TATGGCTCCATTTTAAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCAT 1188

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:14:09 ; Search time 3457.33 Seconds
(without alignments)
10287.096 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
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- 15: em_estfun:*
- 16: em_estom:*
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- 18: em_gss_inv:*
- 19: em_gss_pin:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
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- 23: em_gss_mus:*
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- 26: em_gss_pug:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1191	100.0	1191	29	AY404787 Homo sapi
2	1116.2	93.7	1187	29	AY404788 Pan trogl
3	889.2	74.7	1191	29	AY404789 Mus muscu
4	798.6	67.1	997	13	EX348812 BX348812

C	5	542	45.5	809	14	CD367121
C	6	532	44.7	903	13	BX330186
C	7	481	40.4	721	14	CD365430
C	8	470	39.5	736	14	CD366881
C	9	460.6	38.7	1201	13	BX336527
C	10	438	36.8	496	13	EX097926
C	11	436	36.6	700	14	CD365279
C	12	435	36.5	621	14	CD470995
C	13	420	35.3	660	12	BM726245
C	14	419	35.2	542	12	BM264098
C	15	416.2	34.9	660	10	BF667988
C	16	405.6	34.1	553	12	BM258181
C	17	405	34.0	829	10	BE958211
C	18	397.6	33.4	726	14	CF739045
C	19	392	32.9	499	12	BI773943
C	20	387	32.5	650	14	CD366344
C	21	386	32.4	474	12	BM105642
C	22	382	32.1	532	14	CD536450
C	23	364.2	30.6	498	14	CB221964
C	24	354	29.7	588	12	BM680856
C	25	354	29.7	807	10	BF167811
C	26	344.8	29.0	475	10	BF654980
C	27	342.6	28.8	458	14	CD464412
C	28	334.8	28.1	572	13	BX511990
C	29	321	27.0	635	14	CD470023
C	30	313.8	26.3	533	10	BE502961
C	31	312	26.2	526	12	BG232061
C	32	303.2	25.5	588	14	CD465714
C	33	300.2	25.2	588	14	CD470028
C	34	299.8	25.2	572	14	CD470901
C	35	299.8	25.2	585	14	CD464304
C	36	299.2	25.1	368	10	BF706009
C	37	299	25.1	518	9	AI392922
C	38	298.2	25.0	584	14	CD536362
C	39	293.2	24.6	587	14	CD464888
C	40	284.6	23.9	551	14	CD464476
C	41	280.6	23.6	497	10	AW213499
C	42	256.4	21.5	528	12	BG235994
C	43	248.6	20.9	265	10	BF899685
C	44	229.8	19.3	853	29	CNS03P70
C	45	229.4	19.3	393	13	BY164857

ALIGNMENTS

RESULT 1	AY404787	1191 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	AY404787	Homo sapiens GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.			
DEFINITION	AY404787	GSS.			
ACCESSION	AY404787.1	GI:39760764			
VERSION	GSS.				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
AUTHORS	1 (bases 1 to 1191) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1191)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM2007"

gene

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.3e-293;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGTGGACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 60

QY 61 TATGTTGAGTACCTGGGGGGTGGTGGCTGTGTGACAGCAGCCGCTGGCAATGTGCTC 120
DB 61 TATGTTGAGTACCTGGGGGGTGGTGGCTGTGTGACAGCAGCCGCTGGCAATGTGCTC 120

QY 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCGTACCCGATTCACCTGCTCATAGCC 180
DB 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCGTACCCGATTCACCTGCTCATAGCC 180

QY 181 AACCTACAGTGGTGTATCTCTTACTGACAGCTCTCTGAGCCCTCTCTGTGGACACC 240
DB 181 AACCTACAGTGGTGTATCTCTTACTGACAGCTCTCTGAGCCCTCTCTGTGGACACC 240

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DB 241 TACCTCACCTGACCTGGCGGACCGGTGACCTTCTGAGGATTTTGGGCTCTCCCTT 300

QY 301 TTGCTCTCAATCTGTCTCATCTGACCTCTGCTCATGCTGCTGAGCAGCTACCTC 360
DB 301 TTGCTCTCAATCTGTCTCATCTGACCTCTGCTCATGCTGCTGAGCAGCTACCTC 360

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DB 361 CTCATTGCCACCTAGCTTTTCCCAAGTTTTCAGTCCAGGAGTGTGCTGGCA 420

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DB 421 CTGTGAGCACCTGGGTGTGGGCGTGGCCAGCTTTGCTCCCTCTGGCTATTATATC 480

QY 481 CTGTGACTGTAGTCTGACCTGAGCTTTGACCGATTCGAGGCGGCTTACACACC 540
DB 481 CTGTGACTGTAGTCTGACCTGAGCTTTGACCGATTCGAGGCGGCTTACACACC 540

QY 541 ATCTCATGGGATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCCCT 600
DB 541 ATCTCATGGGATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCCCT 600

QY 601 ATCCACCGCAGGTCAACGAGCAGCAGCAGCAGTGTGAGGCGATCTGCTTTCAGGAG 660
DB 601 ATCCACCGCAGGTCAACGAGCAGCAGCAGCAGTGTGAGGCGATCTGCTTTCAGGAG 660

QY 661 AGATCCACTTCCAACTATGGGCGGCTGATGAGGCGATCTGCTTTCAGGAG 720
DB 661 AGATCCACTTCCAACTATGGGCGGCTGATGAGGCGATCTGCTTTCAGGAG 720

QY 721 CTGACAGCAGGTTAGCATCAGGAGCAGCAGCAGTGTGAGGCGATTTCTAGCAGGTCACT 780
DB 721 CTGACAGCAGGTTAGCATCAGGAGCAGCAGCAGTGTGAGGCGATTTCTAGCAGGTCACT 780

QY 781 GCTGCCACACCCAGACCCCTGGAGGGGACTCATCAGAGTGGAGACCATCAACAGC 840
DB 781 GCTGCCACACCCAGACCCCTGGAGGGGACTCATCAGAGTGGAGACCATCAACAGC 840

QY 841 AAGAGAGCTAGCAGATGCGAGAGAAAGCCCTCCAGAGGATCTGCCAAGAGCCAGCCA 900
DB 841 AAGAGAGCTAGCAGATGCGAGAGAAAGCCCTCCAGAGGATCTGCCAAGAGCCAGCCA 900

QY 901 ATTAAGAGAGCCAGAGAGCTCCGATTTCTCATCGGAATTTGGAGAGTCACTCGAATG 960
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QY 1141 TATGCTCTCATTTTAAAGAGAGGCGCCCGAGTTTCCATAGGCTCCATTAG 1191
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RESULT 2
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LOCUS Pan troglodytes GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY404788
VERSION AY404788.1 GI:39760765
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (bases 1 to 1187)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,W.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1187)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,W.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1..1187
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gene

ORIGIN

Query Match 93.7%; Score 1116.2; DB 29; Length 1187;
Best Local Similarity 94.4%; Pred. No. 4.4e-274;
Matches 1121; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGTGGACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 60

Db 301 TTACTTCCAAATTCGTCTCCATCCTCCTCACCCTCTGTCTCTAGGACGCTACCTC 360
 QY 361 CTCATTGCCACCTTAAGCTTTTCCCAAGATTTTCAGTGCACCAAGGAGTAGTGTGCGCA 420
 Db 361 CTCATTGCCACCTTAAGCTTTTCCCAAGATTTTCAGTGCACCAAGGAGTAGTGTGCGCA 420
 QY 421 CTGGTGACACCTCGGTTGTGGGGTGGCGAGCTTTCCTCCCTCTGCTTATATATC 480
 Db 421 CTGGTGACACCTCGGTTGTGGGGTGGCGAGCTTTCCTCCCTCTGCTTATATATC 480
 QY 481 CTGGTGACACCTCGGTTGTGGGGTGGCGAGCTTTCCTCCCTCTGCTTATATATC 540
 Db 481 TTGGTGCCAGTGTCTGCACCTGAGCTTTGACCGCATGCGAGCGCGCTTACACCACT 540
 QY 541 ATCCTCATGGCAGTCTACTTGTCTTGGGCTCAGCAGTGTGGCATCTTCTATGCTTC 600
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 QY 661 AGCATCCTCCTACACCTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 720
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 QY 1081 CTCATGCT 1140
 Db 1081 CTCATGCT 1140
 QY 1141 TATGGCTCCATTTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1190
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RESULT 4
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 LOCUS
 DEFINITION BX348812 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CSODI029YE18 5-PRIME, mRNA sequence.
 ACCESSION BX348812
 VERSION BX348812.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 997)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6847.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSOBAG028ZC10_CS02667_1&cluster=6847.r.
 Contact: Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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 /note="1st strand cDNA was primed with a NotI-oligo (dr)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Query, Match 67.1%; Score 798.6; DB 13; Length 997;
 Best Local Similarity 98.7%; Pred. No. 6.9e-193;
 Matches 823; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
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 Db 15 GCGTATCTCTCTACTGACGCTCTTTCAGCCCTTCTCTGTGACACCTACCTCCACCT 74
 QY 252 GCATGCGCGCACCGGTGCGACCTTCTGAGGGATTTTGGGCTCTCTTTTGGCTCAA 311
 Db 75 GCATGCGCGCACCGGTGCGACCTTCTGAGGGATTTTGGGCTCTCTTTTGGCTCAA 134
 QY 312 TTCTGTCTCCATCTGACCTCTGCTCATCGCACTGGAGCTACCTCTCATTTGCCCA 371
 Db 135 TTCTGTCTCCATCTGACCTCTGCTCATCGCACTGGAGCTACCTCTCATTTGCCCA 194
 QY 372 CCTAAGCTTTTCCCAAGTTTTCAGTGCACCAAGGGATAGTGTGCACTGTGTAGCAC 431
 Db 195 CCTAAGCTTTTCCCAAGTTTTCAGTGCACCAAGGGATAGTGTGCACTGTGTAGCAC 254
 QY 432 CTGGGTTGTGGGCTGCGGAGCTTTGCTCCCTCTGGCTATTATATCTGTGTACCTGT 491
 Db 255 CTGGGTTGTGGGCTGCGGAGCTTTGCTCCCTCTGGCTATTATATCTGTGTACCTGT 314
 QY 492 AGTCTGACCTGCACTGAGCTTTGACCGCATCCGAGGCGGCTTACACCACTCTCATGGG 551
 Db 315 AGTCTGACCTGCACTGAGCTTTGACCGCATCCGAGGCGGCTTACACCACTCTCATGGG 374
 QY 552 CATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATGCTGTATCCACGCCA 611
 Db 375 CATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATGCTGTATCCACGCCA 434
 QY 612 GGTCAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACGAGCAAGCACTC 671
 Db 435 GGTCAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACGAGCAAGCACTC 494
 QY 672 CAACCATGTGCGCAGCAGTGTGAGGCGCATGCTGTGCTTCCAGAGTGTGAGCAGCAG 731
 Db 495 CAACCATGTGCGCAGCAGTGTGAGGCGCATGCTGTGCTTCCAGAGTGTGAGCAGCAG 554
 QY 732 GTTAGCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 791
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615 CCAGACCCCTGGAGGAGCTCATCAGAGTGGAGACCGATCAACAGCAGAGAGCTAA 674
852 GCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCCGACCAATTAAGGAGC 911
675 GCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAG-CCAGCCCAATTAAGGAGC 733
912 CAGAGAGCTCGGATCTTCATCGGAATTTGGGAGGAGTCACTCGAATGTGTTTGGCTGT 971
734 CAGAAGAGTNGNATTTCTATCGGATTTGGGAGGAGTCACTCGAATGTGTTTGGCTGT 973
972 GTTCTCTCTGTTGGCCCTGAGCTACATCCCC-TTCTTGCTGCTCAACATTCCTGG 1024
794 GTTCTCTCTGTTGGCCCTGAGCTACATCCCCCTTCTTGCTGCTTAACATTCCTG 847

RESULT 5
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LOCUS
DEFINITION
UI-H-FT2-bjp-1-20-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjp-1-20-0-UI 3', mRNA sequence.
CD367121
CD367121.1 GI:31151211
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 809)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
Location/Qualifiers
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/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
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NCI CGAP FT2 is a subcloned cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
subtracted according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. The tissue was provided by Dr.
Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Aveolar Macrophage
TAG LIB=UI-H-FT2
TAG_SEQ=GGCCATGCGG"

ORIGIN
Query Match 45.5%; Score 542; DB 14; Length 809;
Best Local Similarity 99.1%; Pred. No. 2.6e-127;
Matches 575; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

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809 GGTCAACGAGCGACAGCAGCATGGACC-ATACAGTTGCGACAGGACGATCCACTC 751
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690 GTTAGCATCAGGAGGACCCAGTGAAGGATTTATCTGAGCCAGTCACTGCTGCTCCACAC 633
792 CCAGACCTCGAAGGAGTCACTCAGAGTGGGAGACCATCAACAGCAGAGAGAGCTAA 851
632 CCAGACCTCGAAGGAGTCACTCAGAGTGGGAGACCATCAACAGCAGAGAGAGCTAA 573
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1032 AGTCCAGGCTCCCGGAGTGGTCCATGCTGTTGCTGCCAATCTACCTGGCTCAATGGTTG 1091
392 AGTCCAGGCTCCCGGAGTGGTCCATGCTGTTGCTGCCAATCTACCTGGCTCAATGGTTG 333
1092 CATCAACCTCTGCTCTATGAGCAGCATGACCGGCAATTCGCGCAAGCATATGCTCCAT 1151
332 CATCAACCTCTGCTCTATGAGCAGCATGACCGGCAATTCGCGCAAGCATATGCTCCAT 273
1152 TTTAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
272 TTTAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 233

BX330186 903 bp mRNA linear EST 01-MAY-2003
BX330186 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1029YE18 3-PRIME, mRNA sequence.
BX330186
BX330186.1 GI:30307910
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 903)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6847.r For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAK055DE01NM
1&cluster=6847.r. Contact : Peng Liang Email : liang@lifetech.com
URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0BAK055DE01NM1.

FEATURES
Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN	Query Match	44.7%;	Score 532;	DB 13;	Length 903;
	Best Local Similarity	97.8%;	Pred. No. 1e-124;		
	Matches 538;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;
Qy	642 ATCAAGTTGGACAGGCAAGCATCCACTCAACATGTGGCCAGGACTGATGAGGCCAT	701			
Db	757 ATCCAGTTGGCGGAGGCAAGCATCCACTCAACATGTGGCCAGGACTAATGAGGCCAA	698			
Qy	702 GCCTGTCGTTTCCAGGAGCTGGACAGAGTTAGCATCAGGAGGCCACCGAGGGGAT	761			
Db	697 GCCTGTCGTTTCCAGGAGCTGGACAGAGTTAGCATCAGGAGGCCACCGAGGGGAT	638			
Qy	762 TTATCTGAGCAGTCACTGCTGCCACACCCAGACCTCGAAGGGGACTCATCAGAAGT	821			
Db	637 TTATNTGAGCCAGTCACTGCTGCCACACCCAGACCTCGAAGGGGACTCATCAGAAGT	578			
Qy	822 GGGAGACAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGC	881			
Db	577 GGGAGACAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGC	518			
Qy	882 ATCTGCCAAAGCCAGCCAAATTAAGAGAGCCAGAGAGCTCCGATTTCTTCATCGGAAT	941			
Db	517 ATCTGCCAAAGCCAGCCAAATTAAGAGAGCCAGAGAGCTCCGATTTCTTCATCGGAAT	458			
Qy	942 TGGGAAGTGACTCGAATGTGTTTGTGCTGCTTCTCTGCTTTTCCCTGAGCTACATCCC	1001			
Db	457 TGGGAAGTGACTCGAATGTGTTTGTGCTGCTTCTCTGCTTTTCCCTGAGCTACATCCC	398			
Qy	1002 CTTCTTCTGCTCAACATTTCTGGATGCCAGATCCAGGCTCCCGGGTGTCCACATGCT	1061			
Db	397 CTTCTTCTGCTCAACATTTCTGGATGCCAGATCCAGGCTCCCGGGTGTCCACATGCT	338			
Qy	1062 TGCTGCCAAACCTCACTCGGCTCAATGTTGATCAACCCCTGCTGCTATGCAAGCCATGAA	1121			
Db	337 TGCTGCCAAACCTCACTCGGCTCAATGTTGATCAACCCCTGCTGCTATGCAAGCCATGAA	278			
Qy	1122 CCGCAATTCGCAAGCATATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCATAG	1181			
Db	277 CCGCAATTCGCAAGCATATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCATAG	218			
Qy	1182 GTCCTCATAG	1191			
Db	217 GTCCTCATAG	208			

RESULT 7
 CD365430/c
 LOCUS
 DEFINITION UI-H-PT2-bj1-1-21-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
 UI-H-PT2-bj1-1-21-0-UI 3', mRNA sequence.
 ACCESSION CD365430
 VERSION CD365430.1 GI:31149520
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 721)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 Tumor Gene Index
 Unpublished (1997)
 CONTACT Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.utowa.edu/distribution/cgap.html>
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES	Location/Qualifiers
Source	1..721
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="UI-H-PT2-bj1-1-21-0-UI"
	/tissue_type="Aveolar Macrophage"
	/dev_stage="Adult"
	/lab_hosts="DH10B (Life Technologies)"
	/clone_lib="NCI-CGAP FT2"
	/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG LIB=UI-H-FT2 TAG_SEQ=GGCCATGCGG"

ORIGIN	Query Match	40.4%;	Score 481;	DB 14;	Length 721;
	Best Local Similarity	99.8%;	Pred. No. 9.8e-112;		
	Matches 492;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
Qy	699 CATGCTCGTTCCTTCCAGGAGCTGGACAGAGCTTAGCATCAGGAGGCCAGTGGG	758			
Db	721 CATGCTCGTTCCTTCCAGGAGCTGGACAGAGCTTAGCATCAGGAGGCCAGTGGG	662			
Qy	759 GATTTCATCTGAGCCAGTCAGTGTGCCACCCAGACCCCTGGAAGGGAGCTCATAGA	818			
Db	661 GATTTCATCTGAGCCAGTCAGTGTGCCACCCAGACCCCTGGAAGGGAGCTCATAGA	603			
Qy	819 AGTGGAGACAGATCAACAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGA	878			
Db	602 AGTGGAGACAGATCAACAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGA	543			
Qy	879 AGCATCTCCAAAGCCAGCCAAATTAAGGAGCCAGAGAGCTCCGATTTTCATCGGA	938			
Db	542 AGCATCTCCAAAGCCAGCCAAATTAAGGAGCCAGAGAGCTCCGATTTTCATCGGA	483			
Qy	939 ATTTGGGAGGTGACTCGAATGCTTTTGTGCTTCTCTGCTTTCCTGAGCTACAT	998			
Db	482 ATTTGGGAGGTGACTCGAATGCTTTTGTGCTTCTCTGCTTTCCTGAGCTACAT	423			
Qy	999 CCGCTTCTTGTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGTCCACAT	1058			
Db	422 CCGCTTCTTGTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGTCCACAT	363			
Qy	1059 GCTTGTGCGCAACCTCAGCTGCTCAATGTTGATGATCAACCTGCTGCTATGAGCCAT	1118			
Db	362 GCTTGTGCGCAACCTCAGCTGCTCAATGTTGATGATCAACCTGCTGCTATGAGCCAT	303			
Qy	1119 GAACCGCAATTCGCCCAAGCATATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCCA	1178			
Db	302 GAACCGCAATTCGCCCAAGCATATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCCA	243			
Qy	1179 TAGCTCCATTAG	1191			
Db	242 TAGCTCCATTAG	230			

RESULT 8
 CD365881/c
 LOCUS
 DEFINITION UI-H-FT2-bj1-k-21-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone

UI-H-FT2-bjp-k-21-0-UI 3', mRNA sequence.
CD366881
CD366881.1 GI:31150971
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1. .736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjp-k-21-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/notes="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
subtracted according to Bonaldi, Lennon and Soares, Genome
Research, 6:791-806, 1996. The tissue was provided by Dr.
Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Aveolar Macrophage
TAG LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

FEATURES
source

ORIGIN	Query Match	Best Local Similarity	Matches	39.5%	Score	470;	DB	14;	Length	736;
			Conservative	0;	Mismatches	1;	Indels	3;	Gaps	3;
Qy	685	AGGACTCATCAGGCCATGCTGTGCTGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGA	744							
Db	736	AGGACTCATCAGGNCATGCTGTGTGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGA	677							
Qy	745	GGACCCAGTCAGGGGATTTTCATCTGAGCCAGTCAGTGTCTGCCACCCACAGACCCCTGGAA	804							
Db	676	GGACCCAGTGA-GGGATTTTCATCTGAGCCAGTCAGTGTCTGCCACCCACAGACCCCTGGAA	618							
Qy	805	GGGAGCTCATCAGAAGTGGAGACCAAGTCAACACGCAAGAGAGCTAAGCAGATGGCAGAG	864							
Db	617	-GGGACTCATCAGAAGT-GGAGACCAAGTCAACACGCAAGAGAGCTAAGCAGATGGCAGAG	560							
Qy	865	AAAAGCCCTCCAGAAGCATCTGCCAAGAGCCAGCCAAATTAAAGAGAGCCAGAAAGCTCCG	924							
Db	559	AAAAGCCCTCCAGAAGCATCTGCCAAGAGCCAGCCAAATTAAAGAGAGCCAGAAAGCTCCG	500							
Qy	925	GATTCITTCATCGGAATTTGGGAAGGTGACTCGAAATGTGTTTGCTGTGTTTCTCTGCTTT	984							
Db	499	GATTCITTCATCGGAATTTGGGAAGGTGACTCGAAATGTGTTTGCTGTGTTTCTCTGCTTT	440							
Qy	985	GCCCTGAGCTACATCCCTCTTCTGCTCTCAACATTCGTGATGCCAGATCCAGGCTCCC	1044							
Db	439	GCCCTGAGCTACATCCCTCTTCTGCTCTCAACATTCGTGATGCCAGATCCAGGCTCCC	380							

Qy	1045	CGGGTGGTCCACATGCTTCTGTCGCAACCTCACCTGGTCAATGGTTGCATCAACCCGTGTG	1104
Db	379	CGGGTGGTCCACATGCTTGTGTCGCAACCTCCTGGTCAATGGTTGCATCAACCCGTGTG	320
Qy	1105	CTCATGACGCCATGAACCGCCCAATTCGCCCAAGCATATATGGCTCCCAATTTTAAAAAGAGGG	1164
Db	319	CTCATGACGCCATGAACCGCCCAATTCGCCCAAGCATATGGCTCCCAATTTTAAAAAGAGGG	260
Qy	1165	CCCGGAGTTTCCATAGGCTCCCAATTAG	1191
Db	259	CCCGGAGTTTCCATAGGCTCCCAATTAG	233

RESULT 9
BX336527
LOCUS
DEFINITION
1201 bp mRNA linear EST 02-MAY-2003
BX336527 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone SCODIO29YE18 5-PRIME, mRNA sequence.
ACCESSION
BX336527
VERSION
BX336527.1 GI:30341523
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
AUTHORS
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope

BP 191 91006 EVRY cedex - France
Email: segrif@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6847.f For
more information about this cluster, see
<http://www.genoscope.cns.fr/>
<http://bin/cluster.cgi?seq=CS0D1029BC03QPI&cluster=6847.f>. Contact :
Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1029BC03QPI.

FEATURES	source
Location/Qualifiers	
1. 1201	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="CS0D1029YE18"	
/tissue_type="PLACENTA COT 25-NORMALIZED"	
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"	
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	

ORIGIN	Query Match	38.7%; Score 460.6; DB 1.3; Length 1201;
	Best Local Similarity	77.7%; Pred. No. 2.2e-106;
	Matches 678; Conservative	62; Mismatches 96; Indels 37; Gaps 16
Qy	5	GGAACAGCTCTG-ACGCCAATCTCTCTGTAACC--ATGAGCTCTGCT-GGGCTATCGT 60
Db	105	GGAAMAGCTCTGTAGCCCAATTTCTCTGTACCTATGGAGTCTGTGTCGCGGTACWGCT 164
Qy	61	TATGTTTCAGTTAGCTGGGGGGTGGTGGTCTGTACAGGCACCGTGGGCAATGTGTC 120
Db	165	TATGTTTCAGTTAGCTGGGGGGTGGTGGTCTGTACAGMACCGTGGGCAATGTGTC 224
Qy	121	ACCCTACTGGGCTTG-GCCATCCAGCCCAAGCTCCGTAACCGATTCT--AACTGCTGCATA 177
Db	225	AMCMTACTGGGCTTGTGCATCCAGCCCAAGCTCCGTAACCGATTCTAATCTGCTGCATA 284
Qy	178	GCCAACTTCACACTGGGCTGAT-----CTCCCTCTACTGCACGCTC---CTTCAGGCCCTTCT 229

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 700)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
 Seq primer: M13 FORWARD
 POLYA=Yes.

Location/Qualifiers
 1..700
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-F12-bj-j-k-21-0-UI"
 /tissue_type="Aveolar Macrophage"
 /dev stage="Adult"
 /lab host="DH10B (Life Technologies)"
 /clone lib="NCI CGAP FT2"
 /notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT2 is a subcloned cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_LIB=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-F12
 TAG_SEQ=GGCCATGCCG"

FEATURES
 source
 1..700
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-F12-bj-j-k-21-0-UI"
 /tissue_type="Aveolar Macrophage"
 /dev stage="Adult"
 /lab host="DH10B (Life Technologies)"
 /clone lib="NCI CGAP FT2"
 /notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT2 is a subcloned cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_LIB=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-F12
 TAG_SEQ=GGCCATGCCG"

ORIGIN
 36.6%; Score 435; DB 14; Length 700;
 Best Local Similarity 98.9%; Pred. No. 3.1e-100; Mismatches 2; Indels 3; Gaps 3;
 Matches 469; Conservative 0;

QY 718 GAGCTGGACGAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCTCTGAGCCAGTC 777
 Db 700 GAGCTGGACGAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCTCTGAGCCAGTC 642
 QY 778 AGTGCTGCCACCCAGACCCCTGGAGGGGACTCATCAGAGTGGAGCCAGATCAAC 837
 Db 641 AGT-CTGCCACCCAGACCCCTGGAA-GGGACTCATCAGAGTGGAGCCAGATCAAC 584
 QY 838 AGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGAGCATCTGCCAAAGCCAG 897
 Db 583 AGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGAGCATCTGCCAAAGCCAG 524
 QY 898 CCAATTAAAGGAGCCAGAGAGCTCCGATTTCTTCATCGGAATTGGGAAGTGACTCGA 957
 Db 523 CCAATTAAAGGAGCCAGAGAGCTCCGATTTCTTCATCGGAATTGGGAAGTGACTCGA 464
 QY 958 ATGTGTTTCTGTTCTCTCTCTGTTGCTGCTGAGCTACATCCCTCTTCTGCTGCTCAAC 1017
 Db 463 ATGTGTTTCTGTTCTCTCTGTTGCTGCTGAGCTACATCCCTCTTCTGCTGCTCAAC 404
 QY 1018 ATTCTGGATGCCAGATCCAGGCTCCCGGGTGGTCCACATGTTCTGCCAACCTCACC 1077
 Db 403 ATTCTGGATGCCAGATCCAGGCTCCCGGGTGGTCCACATGTTCTGCCAACCTCACC 344
 QY 1078 TGGCTCAATGGTTGCATCAACCTGTCTATGAGGATCAACCGCCAAATTCGCCCA 1137
 Db 343 TGGCTCAATGGTTGCATCAACCTGTCTATGAGGATCAACCGCCAAATTCGCCCA 284

QY 1138 GCATATGGCTCCATTATAAAGAGGCGCCCGAGTTTCCATAGGCTCCATTAG 1191
 Db 283 GCATATGGCTCCATTATAAAGAGGCGCCCGAGTTTCCATAGGCTCCATTAG 230

RESULT 12
 LOCUS CD470995 621 bp mRNA linear EST 04-JUN-2003
 DEFINITION LeukoS5_3_D04.g1_A027 Stimulated peripheral blood leukocytes S5
 Equus caballus cDNA clone LeukoS5_3_D04_A027 5', mRNA sequence.
 ACCESSION CD470995
 VERSION CD470995.1 GI:31392263
 KEYWORDS EST.
 SOURCE Equus caballus (horse)
 ORGANISM Equus caballus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 REFERENCE 1 (bases 1 to 621)
 AUTHORS Vandenplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Moore, J. N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L. H.
 TITLE An EST database from equine (Equus caballus) stimulated peripheral blood leukocytes
 JOURNAL Unpublished (2003)
 COMMENT Other ESTs: LeukoS5_3_D04.b1_A027
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1950
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

FEATURES
 source
 1..621
 /organism="Equus caballus"
 /mol_type="mRNA"
 /strain="Bartmoor Pony"
 /db_xref="taxon:9796"
 /clone="LeukoS5_3_D04_A027"
 /sex="male"
 /tissue_type="blood"
 /cell_type="leukocytes"
 /lab_hosts="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Stimulated peripheral blood leukocytes S5"
 /note="Organ: circulatory system; Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from equine peripheral blood leukocytes isolated from a healthy adult horse. The leukocytes were stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN
 36.5%; Score 435; DB 14; Length 621;
 Best Local Similarity 91.1%; Pred. No. 5.2e-100; Mismatches 45; Indels 0; Gaps 0;
 Matches 462; Conservative 0;

QY 1 ATGTGGGAACAGCTCGACGCCAATTCTCTGTGTACCATGAGTCTGTGGGTATCGT 60
 Db 115 ATGTGGGAACAGCTCGATGCCAATTCTCTGTGTACCATGAGTCTGTGGGTATCGT 174
 QY 61 TATGTTGAGTGTAGCTGGGGGTGGTGGTGTGTGACGACCCGTGGGCAATGTGCTC 120


```

Db      175  TACGTTGCAAGTTAGCTGGGGGGTGGTGGCTGTGACAGGACCGTGGGCAACGTCGCTC 234
Qy      121  ACCCTACTGCGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACACCTGCTCATAGCC 180
Db      235  ACCCTGCTGGCTTGGCCATCCAGCCCAAGCTCCGTACCTGCTTCAACCTGCTCATGCC 294
Qy      181  AACCTACACTGGCTGATCTCTCTACTGACAGCTCTTCCAGCCCTCTCTGTTGGACAC 240
Db      295  AATCTCAGTGGCCGATCTCTCTACTGACCCCTTCTCCAGCCCTTCTCGGTGGACAC 354
Qy      241  TACCTCCACTGCACTGGCCGACCGGTGCGACCTTCTGACAGGCTATTGCGCTCTCTCT 300
Db      355  TACCTCCACTGCACTGGCCGACCGGTGCGACCTTCTGACAGGCTATTGCGCTCTCTCT 414
Qy      301  TTTGCTCTCAATCTGTCTCACTGACCTCTGCTCTGCTCTGCTCTGCTGACGACCTACCTC 360
Db      415  TTTGCTCTCAATCTGTCTCACTGACCTCTGCTCTGCTCTGCTCTGCTGACGACCTACCTC 474
Qy      361  CTCATTGCGCCACCTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGAGTAGTCTGGCA 420
Db      475  CTCATTGCGCCACCTAAGCTTTTCCCAAGTTTTCAGTCCCAAGGAGTAGTCTGGCA 534
Qy      421  CTGCTGAGCACCTGGGTGTGGGGTGGCCAGCTTTGCTCCCTCTGCTGGCTATTATATC 480
Db      535  CTGCTGAGCACCTGGGTGTGGGGTGGCCAGCTTTGCTCCCTCTGCTGGCCATCTATATC 594
Qy      481  CTGCTGAGCACCTGGGTGTGGGGTGGCCAGCTTTGCTCCCTCTGCTGGCTATTATATC 507
Db      595  TTGCTGCGCGTAGTTGCACTGCGAC 621

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RESULT 13
BM726245 560 bp mRNA linear EST 01-MAR-2002
LOCUS UI-E-EJ0-aih-k-10-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
DEFINITION UI-E-EJ0-aih-k-10-0-UI 5', mRNA sequence.
ACCESSION BM726245
VERSION BM726245.1 GI:19047578
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
1 (bases 1 to 660)
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 599-657, >AT rich#Low_complexity (matched complexity)
Seq primer: M13 Reverse.
FEATURES
source Location/Qualifiers
1..660
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-aih-k-10-0-UI"

```

```

/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/notes="Organ: eye; Vector: pTV73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ0 is a subcloned cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pTV73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene discovery in the
Visual System, supported by National Eye Institute (NEI)."
ORIGIN
Query Match 35.3%; Score 420; DB 12; Length 660;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 772 CCAGTCAGTGTGTCACCAACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACG 831
Db 1 CCAGTCAGTGTGTCACCAACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACG 60
Qy 832 ATCAACACAGAGAGCTTAAGCAGATGCGAGAGAAAGCCCTCCAGAGCATCTGCCAAA 891
Db 61 ATCAACACAGAGAGCTTAAGCAGATGCGAGAGAAAGCCCTCCAGAGCATCTGCCAAA 120
Qy 892 GCCCAGCCAAATTAAGGAGCCAGAGAGCTCCGGAATCTTCATCGGAATTTGGGAAGTG 951
Db 121 GCCCAGCCAAATTAAGGAGCCAGAGAGCTCCGGAATCTTCATCGGAATTTGGGAAGTG 180
Qy 952 ACTCGAATGTGTTTGTGCTGTTCTCTGCTTTGCCCTGAGCTACATCCCTCTTGTCTG 1011
Db 181 ACTCGAATGTGTTTGTGCTGTTCTCTGCTTTGCCCTGAGCTACATCCCTCTTGTCTG 240
Qy 1012 CTCACATCTTGGATGCGAGAGTCCAGCTCCCGGGTGGTCCACATGCTTGTGCTCAAC 1071
Db 241 CTCACATCTTGGATGCGAGAGTCCAGCTCCCGGGTGGTCCACATGCTTGTGCTCAAC 300
Qy 1072 CTCACCTGGCTCAATGTTGTCATCAACCTGCTCTATGAGCCATCAACCGCAATTC 1131
Db 301 CTCACCTGGCTCAATGTTGTCATCAACCTGCTCTATGAGCCATCAACCGCAATTC 360
Qy 1132 CGCCAAGCATATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGCTCCATTAG 1191
Db 361 CGCCAAGCATATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGCTCCATTAG 420

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RESULT 14
 BM254098 542 bp mRNA linear EST 17-DEC-2001
 LOCUS 515432 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION BM254098
 ACCESSION BM254098
 VERSION BM254098.1 GI:17889697
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 542)
 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,

Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
 Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F.,
 Quackenbush, J., and Keel, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine CDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)

TITLE

JOURNAL
 MEDLINE
 PUBMED

COMMENT

Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68333-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers

FORWARD: AGAAACAGCTATGACCAT
 BACKWARD: GTTTCACGTCAGCAGC
 Plate: 113 row: O column: 5
 Seq primer: ATTAGGTGACACTATAG.

FEATURES

Source

1. 542
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 3B0V"
 /note="Vector: pCMV SP076; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from marrow, alveolar
 macrophage, ovary, fetal semitendinosus muscle, and fetal
 longissimus muscle."

ORIGIN

Query Match 35.2%; Score 419; DB 12; Length 542;
 Best Local Similarity 86.9%; Pred. No. 5.9e-96;
 Matches 472; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

QY 576 CAGTGTGGCATCTTCTATTGCTCATCCACCGCAGGTCAACGAGCAGCAGCAGCAGT 635
 DB 1 CAGTGTGGGTGCTTCTATTGCTCATCCACCGCAGGTGAAGCGCAGCAGCAGCAGT 60

QY 636 GGCACCATACAGTTCGGCAGCAGCATCCATCCACCATGTGGCCAGCAGTATGATCA 695
 DB 61 GAATCATGACAGCTGGCGCAGCAAGCATCCGTTCCAAACCATGTGGTGGGGCAGCAG 120

QY 696 GGCCATGCTGCTGCTGCTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGCAGCAGTGA 755
 DB 121 GGCGGTGCTGCTGCTGCTTCCAGGAGCTAGACAGTGGGCTGGCATCAGGAGGAGCAGCAG 180

QY 756 GGGGATTTCTATGAGCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 815
 DB 181 GGGGATTTCTATGAGCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 816 AGAAGTGGGAGCAGCATCAACAGCAAGAGAGTAAAGCAGATGGCAGAGAAAGCCCTCC 875
 DB 241 AGAAGTGGGAGCAGCATCAACAGCAAGAGAGTAAAGCAGATGGCAGAGAAAGCCCTCC 300

QY 876 AGAAGCATCTGCCAAGCCAGCCCAATTAAGAGCCAGAGAGTCCGAGTCTTCTTCATC 935
 DB 301 AGGAGTGGCTGCCAAGCCAGCAGCAACTAAAGAGCCAGAGAGTCTCAGGACTCTCCATC 360

QY 936 GGAATTTGGAGAGTCTGATGTTTGTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 995
 DB 361 AGAGTTTGGAGAGT - ACCCGAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 419

QY 996 CATCCCTTTTGTGCTCTCAACATTTCTGGATGCGCAGAGTCCAGGTTCCCGGGTGGTCCA 1055
 DB 420 CATCCCTTTTGTGCTCTCAACATCTGGATGCGCAGAGTCCAGGTTCCCGGGTGGTCCA 479

QY 1056 CATGCTTGTCGCAACCTCACCTGGGCTCAATGGTTGCATCAACCCCTGTCTCTATGCAGC 1115

DB 480 CATGCTGCTGCCAACCTACCTGGCTTAATGGTGCATCAACCTGTGCTGTACGCAGC 539
 QY 1116 CAT 1118
 DB 540 CAT 542

RESULT 15

BF667988

LOCUS

DEFINITION 602122233F1 NIH_MGC_56 Homo sapiens CDNA clone IMAGE:4279185 5',
 mRNA sequence.

ACCESSION BF667988

VERSION BF667988.1 GI:11941883

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 660)

AUTHORS NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: csapbs@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM104 row: a column: 10

High quality sequence stop: 597.

FEATURES

source

1. 660
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4279185"
 /tissue_type="primitive neuroectoderm"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 56"
 /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggcgctggcc); Site 2: SfiI (ggcattatgccc);
 Double-stranded CDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCCGCGCCGACATG-3' (30)EN-3',
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 34.9%; Score 416.2; DB 10; Length 660;
 Best Local Similarity 95.9%; Pred. No. 3.5e-95;
 Matches 492; Conservative 0; Mismatches 13; Indels 8; Gaps 6;

QY 1 ATGTGGAACAGCTCTGACGCC-AACTTCTCTGTGTACCATGAGTCTGTGCTGGCTATCG 59
 DB 102 ATGTGGAACAGCTCTGACGCCCTACTTCTCTGTGTACCATGAGTCTGTGCTGGCTATCG 161

QY 60 TTATGTTTCAGTTAGCTGGGGGTGGTGGTGTGCACAGGC-ACCGTGGGCAATGTGC 118
 DB 162 TTATGTTTCAGTTAGCTGGGGGTGGTGGTGTGCACAGGCCTACCGTGGGCAATGTGC 221

QY 119 TCACCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACTGCTCATAG 178
 DB 222 TCACCTACTGGCTTGGCAATCCAGCCCAAGCTCCGTACCCGATTCAACTGCTCATAG 281

Qy	179	CCAACTTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGCCCTTCTCTGTGGACA	238
Db	282	CCAACTTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGCCCTTCTCTGTGGACA	341
Qy	239	CCTACCTCCACCTGCACTGGGGACCGGTGGCCACCTTCTGACGGT-ATTGGGCTCCTC	297
Db	342	CCTACCTCCACCTGCACTGGGGACCGGTGGCCACCTTCTGACGGT-ATTGGGCTCCTC	401
Qy	298	CTTTTGGCTCCCAATTCTGTCTCCATCCTGACCCCTCTGCTCATCGCACTGGGACGCTAC	357
Db	402	CTTTTGGCTCCCAATTCTGTCTCCATCCTGACCCCTCTGCTCATCGCACTGGGACGCTAC	461
Qy	358	CTCCTCATTTGCCACACCTTAAGCTTTTCCCCAAAGTTTTCAGTCCCAAGGGGATAGTCTG	417
Db	462	CTCCTCATTTGCCACACCTTAAGCTTTTCCCCAAAGTTTTCAGTCCCAAGGGGATAGTCTG	521
Qy	418	G-CACCTGGTGAGCACCTGGGTTGTGGCGTGGCAGCTTTGCTCCCTCTGGGCTATTTA	476
Db	522	GCCACTGGTGAGCACCTGGGTTGTGGCGTGGCAGCTTTGCTCCCTCTGGGCTATTTA	578
Qy	477	TATCCTGGTACCTGTAGTCTGCACTGCACTT	509
Db	579	TATCCTGGTA-CTGTAGTCTGCACTGGGTTT	610

Search completed: September 24, 2004, 04:48:26
 Job time : 3459.33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 04:48:37 ; Search time 133 Seconds
(without alignments)
841.269 Million cell updates/sec

Title: US-10-029-436-2
Perfect score: 2041
Sequence: 1 MNSSDANFSCYHESVLGYR.....PRQAYGSILKEGPRSFHRLH 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04: *
1: Geneseq1980s: *
2: Geneseq1990s: *
3: Geneseq2000s: *
4: Geneseq2001s: *
5: Geneseq2002s: *
6: Geneseq2003as: *
7: Geneseq2003bs: *
8: Geneseq2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2041	100.0	396	2	Aaw62598 Human 7-t
2	2041	100.0	396	4	Aag77798 Human EX3
3	2041	100.0	396	5	Aag80225 Human MAR
4	2041	100.0	396	5	Abp95618 Human GPC
5	2041	100.0	396	6	Abj19755 Human MP2
6	2041	100.0	396	6	Abp81705 Human G p
7	2041	100.0	396	6	Abb82500 Human TGR
8	2041	100.0	396	6	Abx82422 Human hpl
9	2041	100.0	404	4	Aam99936 Human exp
10	1748	85.6	396	6	Abb82509 Mouse TGR
11	570	27.9	115	4	Aam87595 Human inm
12	568	27.8	124	5	Abb89377 Human pol
13	454	22.2	116	4	Aau18097 Novel hum
14	454	22.2	116	4	Aau18646 Renal and
15	454	22.2	116	4	Aau21583 Novel hum
16	454	22.2	116	4	Aam99963 Human exp
17	454	22.2	116	4	Abb10174 Human cDN
18	454	22.2	116	4	Aau87123 Novel cen
19	454	22.2	116	4	Aau18292 Human end
20	454	22.2	116	5	Abj05724 Novel hum
21	454	22.2	116	5	Abp66761 Human hum
22	454	22.2	116	5	Abu97261 Human pol
23	454	22.2	116	7	Adc46224 Human neo
24	378	18.5	634	4	Abb60554 Drosophil
25	373	18.3	633	7	Aae38154 Fruit fly

ALIGNMENTS

RESULT 1

AAW62598
ID AAW62598 standard; protein; 396 AA.
XX
AC AAW62598;
XX
DT 07-OCT-1998 (first entry)
XX
DE Human 7-transmembrane receptor, HNFJD15.
XX
KW G-protein coupled receptor; HNFJD15; treatment; diagnosis; infection;
KW HIV-1; HIV-2; cancer; screening; human; 7-transmembrane receptor;
KW Parkinson's disease; vaccine.
XX
OS Homo sapiens.
XX
PN EP853125-A2.
XX
PD 15-JUL-1998.
XX
PF 20-NOV-1997; 97EP-00309347.
XX
PR 09-JAN-1997; 97US-00775428.
XX
PA (SMIX) SMITHKLINE BEECHAM CORP.
XX
PI Sathe GM, Fuetterer WS, Bergsma DJ, Ellis C;
XX
DR WPI; 1998-364650/32.
XX
N-PSDB; AAV38513.

Human G-protein coupled receptor, HNFJD15 - used e.g. in treatment and diagnosis of infections e.g. by HIV-1, HIV-2 and cancers and screening of antagonistic or agonistic compounds.
Claim 15; Fig 1; 19pp; English.
This represents a human 7-transmembrane receptor, HNFJD15. HNFJD15 is a human G-protein coupled receptor and can be used in vaccines to protect mammals from infections e.g. bacterial, fungal, protozoan and viral infections (especially infections caused by HIV-1 or HIV-2), cancers and Parkinson's disease. The HNFJD15 polypeptides can be used to produce antibodies which are used to treat such infections, isolate or identify clones expressing the polypeptide or to purify the polypeptide. The polypeptides can also be used to screen for compounds binding to, activating or inhibiting activation of HNFJD15. They can be used to diagnose diseases and susceptibility to diseases related to expression or activity of HNFJD15

26 338 16.6 386 4 ABB59683
27 338 16.6 386 4 AAU38928
28 338 16.6 386 7 ADC35766
29 338 16.6 386 4 AAU09940
30 309 15.1 572 4 ABB60541
31 293.5 14.4 414 2 AAR11800
32 293.5 14.4 414 6 ABB62490
33 290.5 14.2 515 2 AAB59668
34 290 14.2 443 2 AAR05541
35 290 14.2 443 2 AAR11497
36 290 14.2 443 2 AAY01600
37 290 14.2 443 4 AAU76292
38 290 14.2 443 4 AAB69075
39 290 14.2 443 5 AAM51019
40 290 14.2 443 6 ADA83796
41 290 14.2 443 6 ABP81809
42 290 14.2 443 6 ABG73545
43 290 14.2 443 6 ABU62489
44 290 14.2 445 7 ADC86205
45 288.5 14.1 497 5 ABB04302

Abb59683 Drosophil
Aau38928 Drosophil
Adc35766 Drosophil
Aau09940 Drosophil
Abb60541 Drosophil
Aar11800 Human rec
Aau62490 Human pit
Aab59668 Hamster a
Aar05541 Human pit
Aar11497 Hman dopa
Aay01600 Human pit
Aau76292 Human D2
Aab69075 Human dop
Aam51019 Human D2
Ada83796 Human DRD
Abp81809 Human dop
Abg73545 Human pit
Abu62489 Human pit
Adc86205 Human GPC
Abb04302 Hamster w

XX Sequence 396 AA;
 Query Match 100.0%; Score 2041; DB 2; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1e-200;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGVGNVLTLLALATQPKLRTFRNLLIA 60
 DB 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGVGNVLTLLALATQPKLRTFRNLLIA 60
 QY 61 NLTADLLYCTLLQFFSVDTYHLHWRGTGATFCRVFGLLFASNSVILTLCLIALGRYL 120
 DB 61 NLTADLLYCTLLQFFSVDTYHLHWRGTGATFCRVFGLLFASNSVILTLCLIALGRYL 120
 QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCFDRIRGRPYTT 180
 DB 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCFDRIRGRPYTT 180
 QY 181 ILMGIFYVLGLSSVGIYFCLIHQVKRAQAALDOYKLRQASIHNSHVARTDEAMPGRFQE 240
 DB 181 ILMGIFYVLGLSSVGIYFCLIHQVKRAQAALDOYKLRQASIHNSHVARTDEAMPGRFQE 240
 QY 241 LDSRLASGSPSEGISSEPFVSAATTQTLEGDSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 DB 241 LDSRLASGSPSEGISSEPFVSAATTQTLEGDSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 QY 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIPFLLNLILDARVOAPRVVHMLAANLTW 360
 DB 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIPFLLNLILDARVOAPRVVHMLAANLTW 360
 QY 361 LNCINPVLVYAMNRQFRQAYGSLKRGPRSFHRLH 396
 DB 361 LNCINPVLVYAMNRQFRQAYGSLKRGPRSFHRLH 396

RESULT 2
 AAG77798
 ID AAG77798 standard; protein; 396 AA.
 AC AAG77798;
 DT 29-JAN-2002 (first entry)
 DE Human EX33 G-protein coupled receptor polypeptide.
 KW G-protein coupled receptor; EX33; rheumatoid arthritis;
 KW neutrophil-associated inflammatory disease; Crohn's disease;
 KW ulcerative colitis; chronic obstructive pulmonary disease; COPD;
 KW adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
 KW inflammatory bowel disease; human; GPCR.
 OS Homo sapiens.
 PN WO200166597-A2.
 XX 13-SEP-2001.
 PF 05-MAR-2001; 2001WO-EP002462.
 PR 06-MAR-2000; 2000US-00518832.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 FI Jarai G, Cooper PR, Yousefi S;
 DR WPI; 2001-541917/60.
 DR N-PSDB; AAH78712.
 XX Use of an inflammatory related G-protein coupled receptor (EX33), a
 PT polynucleotide encoding it or other compounds (e.g. antibodies) in the
 PT diagnosis or treatment of a neutrophil-associated inflammatory disease,

PT e.g. rheumatoid arthritis.
 XX Claim 1; Page 29-30; 32pp; English.
 CC The present amino acid sequence represents EX33, a human inflammatory
 CC disease-related G-protein coupled receptor (GPCR). G-protein coupled
 CC receptors are important targets in therapeutic applications because they
 CC are involved in a wide variety of physiological and pathological
 CC processes. The invention comprises the use of the EX33 polypeptide and
 CC polynucleotide in the diagnosis or treatment of a neutrophil-associated
 CC inflammatory disease. The EX33 polypeptide, EX33 polynucleotide, an
 CC antibody specific to the EX33 polypeptide, and an antisense
 CC oligonucleotide/polynucleotide probe specific to the EX33 polynucleotide
 CC are useful in the diagnosis or treatment of neutrophil-associated
 CC inflammatory diseases, such as chronic obstructive pulmonary disease
 CC (COPD), adult respiratory distress syndrome (ARDS), rheumatoid arthritis,
 CC and inflammatory bowel diseases (e.g., Crohn's disease and ulcerative
 CC colitis)
 XX Sequence 396 AA;
 SQ Query Match 100.0%; Score 2041; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1e-200;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGVGNVLTLLALATQPKLRTFRNLLIA 60
 DB 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGVGNVLTLLALATQPKLRTFRNLLIA 60
 QY 61 NLTADLLYCTLLQFFSVDTYHLHWRGTGATFCRVFGLLFASNSVILTLCLIALGRYL 120
 DB 61 NLTADLLYCTLLQFFSVDTYHLHWRGTGATFCRVFGLLFASNSVILTLCLIALGRYL 120
 QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCFDRIRGRPYTT 180
 DB 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCFDRIRGRPYTT 180
 QY 181 ILMGIFYVLGLSSVGIYFCLIHQVKRAQAALDOYKLRQASIHNSHVARTDEAMPGRFQE 240
 DB 181 ILMGIFYVLGLSSVGIYFCLIHQVKRAQAALDOYKLRQASIHNSHVARTDEAMPGRFQE 240
 QY 241 LDSRLASGSPSEGISSEPFVSAATTQTLEGDSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 DB 241 LDSRLASGSPSEGISSEPFVSAATTQTLEGDSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 QY 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIPFLLNLILDARVOAPRVVHMLAANLTW 360
 DB 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIPFLLNLILDARVOAPRVVHMLAANLTW 360
 QY 361 LNCINPVLVYAMNRQFRQAYGSLKRGPRSFHRLH 396
 DB 361 LNCINPVLVYAMNRQFRQAYGSLKRGPRSFHRLH 396

RESULT 3
 AAG80225
 ID AAG80225 standard; protein; 396 AA.
 XX AAG80225;
 DT 22-JAN-2002 (first entry)
 DE Human MAR1 protein.
 KW MAR1; monoamine receptor-1; human; cytostatic; gene therapy; tumour;
 KW psychiatric disorder; transgenic animal; knockout animal.
 OS Homo sapiens.
 PN DE10021474-A1.
 XX 08-NOV-2001.
 PD
 XX

RESULT 5
 ID ABJ19755
 XX ABJ19755 standard; protein; 396 AA.
 AC
 XX
 XX
 DT 03-APR-2003 (first entry)
 XX
 XX Human MP21 protein EX33 SEQ ID No 35.
 DE
 XX Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic;
 XX cell proliferation disorder; MP21.
 KW
 KW
 XX Homo sapiens.
 OS
 XX
 XX WO2003006990-A1.
 PN
 XX
 XX 23-JAN-2003.
 PD
 XX
 XX 10-JUL-2002; 2002WO-US021549.
 PF
 XX
 XX 12-JUL-2001; 2001US-0305017P.
 PR
 XX 10-OCT-2001; 2001US-0328491P.
 PR
 XX 15-FEB-2002; 2002US-0357452P.
 XX
 XX (EXEL-) EXELIXIS INC.
 FA
 XX
 XX Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
 PI
 XX
 XX WPI; 2003-221779/21.
 DR
 XX N-PSDB; ABT17029.
 DR
 XX
 XX Identifying candidate p21 pathway modulator, by contacting an assay
 PT system having modifiers of p21 polypeptide or gene with a test agent to
 PT provide a reference activity in system and detecting test agent-biased
 PT activity.
 XX
 XX Example; Page 121-123; 199pp; English.
 PS
 XX
 XX The invention relates to a novel method for identifying a candidate p21
 CC pathway modulating agent. The novel method comprises contacting an assay
 CC system, comprising a purified MP21 polypeptide (modifier of p21) or
 CC nucleic acid, with a test agent under conditions, so that but for the
 CC presence of a test agent, the assay system provides a reference activity
 CC and detection of test agent-biased activity of the assay system. The
 CC novel method of the invention is useful for identifying a candidate p21
 CC pathway modulating agent. The invention also includes a method for
 CC modulating the p21 pathway of a cell, and a method for diagnosing a
 CC disease e.g. cancer in a patient. The identified modulators are useful in
 CC diagnosis, therapy and pharmaceutical development. The modulators are
 CC useful in a variety of diagnostic and therapeutic applications including
 CC angiogenic, apoptotic and cell proliferation disorders. This sequence
 CC represents an MP21 protein of the invention
 XX
 XX Sequence 396 AA;
 SQ
 Query Match 100.0%; Score 2041; DB 6; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1e-200;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNSSDANFSCYHESVGLGRYVAVSGVVAVTGTGVNLTLLALAIQPKLATRNFLLIA 60
 Db 1 MNSSDANFSCYHESVGLGRYVAVSGVVAVTGTGVNLTLLALAIQPKLATRNFLLIA 60
 QY 61 NLTLADLLCYTLQPPSVDTYLLHWRGTATCRVFGLLFPASNSVSLTCLIALGRYL 120
 Db 61 NLTLADLLCYTLQPPSVDTYLLHWRGTATCRVFGLLFPASNSVSLTCLIALGRYL 120
 QY 121 LIAHPKLFQVFSAGKIVLALVSTWVGVSAPLWPIVILVPVCTCSFDRIRGRPYTT 180
 Db 121 LIAHPKLFQVFSAGKIVLALVSTWVGVSAPLWPIVILVPVCTCSFDRIRGRPYTT 180

QY 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAQALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
 Db 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAQALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
 QY 241 LDSRLASGGPSEGISSEPVSAATTOTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 Db 241 LDSRLASGGPSEGISSEPVSAATTOTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 QY 301 IKGARRAPDSSEFGKVTMCFVFLCPALSYIPPELLNILDARVQAPRVVHMLAANTW 360
 Db 301 IKGARRAPDSSEFGKVTMCFVFLCPALSYIPPELLNILDARVQAPRVVHMLAANTW 360
 QY 361 LNCGINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
 Db 361 LNCGINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
 RESULT 6
 ID ABP81705
 XX ABP81705 standard; protein; 396 AA.
 AC
 XX ABP81705;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 XX Human G protein-coupled receptor EX33 protein SEQ ID NO:585.
 DE
 XX
 XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200261087-A2.
 PN
 XX
 XX 08-AUG-2002.
 PD
 XX
 XX 19-DEC-2001; 2001WO-US050107.
 PF
 XX
 XX 19-DEC-2000; 2000US-0257144P.
 PR
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA
 XX
 XX Burmer GC, Roush CJ, Brown JP;
 PI
 XX
 XX WPI; 2003-046718/04.
 DR
 XX N-PSDB; ABZ42551.
 DR
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 XX Disclosure; Fig 1; 523pp; English.
 PS
 XX
 XX The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB24289 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 396 AA;

Query Match 100.0%; Score 2041; DB 6; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1e-200;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSVGVVAVTGTGVTGNVLTLLALAIQPKLRTFNLLIA 60
 DB 1 MNSSDANFSCYHESVLGYRYVAVSVGVVAVTGTGVTGNVLTLLALAIQPKLRTFNLLIA 60

QY 61 NLTLADLLYCTLLQPFVSDTYLHLHWRGTATFCRVFGLLLFASNSVSLTLCIALGRYL 120
 DB 61 NLTLADLLYCTLLQPFVSDTYLHLHWRGTATFCRVFGLLLFASNSVSLTLCIALGRYL 120

QY 121 LIAHPKLPQVFSAGKIVLALVSTVWGVASFAPLWPIYILVPVCTCFDRIRGRPYTT 180
 DB 121 LIAHPKLPQVFSAGKIVLALVSTVWGVASFAPLWPIYILVPVCTCFDRIRGRPYTT 180

QY 181 ILMGYFVLGLSSVGIFYCLIHQVRAAQAALDOYKLRQASIHNSHVARTDEAMPGRFOE 240
 DB 181 ILMGYFVLGLSSVGIFYCLIHQVRAAQAALDOYKLRQASIHNSHVARTDEAMPGRFOE 240

QY 241 LDSRLASGGPSEGISSEPVSAATTOTLEGDSSEVDQINSKRAKQMAEKSPPEASAKAQP 300
 DB 241 LDSRLASGGPSEGISSEPVSAATTOTLEGDSSEVDQINSKRAKQMAEKSPPEASAKAQP 300

QY 301 IKGARRAPDSSSEFGKVTMCMFAVFLCFALSYIPFLLNILDARVOAPRVVHMLAANLTW 360
 DB 301 IKGARRAPDSSSEFGKVTMCMFAVFLCFALSYIPFLLNILDARVOAPRVVHMLAANLTW 360

QY 361 LNCGINPVLVYAMNRQFQAYGSILKRGPRSFHRLH 396
 DB 361 LNCGINPVLVYAMNRQFQAYGSILKRGPRSFHRLH 396

RESULT 7
 ABB2500
 ID ABB2500 standard; protein; 396 AA.
 XX
 AC ABB2500;
 XX
 DT 22-JAN-2003 (first entry)
 XX
 DE Human TGR35 polypeptide.
 XX
 KW G-protein coupled receptor; GPCR; antipsoriatic; antiinflammatory;
 KW antilipemic; nootropic; neuroprotective; antianemic; antitumor; human;
 KW antiparkinsonian; antilipemic; TGR35; receptor.
 XX
 OS Homo sapiens.
 XX
 FN WO200277001-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 08-MAR-2002; 2002WO-US007171.
 XX

PR 09-MAR-2001; 2001US-00802803.
 PR 16-MAR-2001; 2001US-0276649P.
 PA (TULA-) TULARIK INC.
 PI Tian H, Zhao J, Chen J, Cutler G;
 XX
 XX WPI; 2003-018881/01.
 DR N-PSDB; ABV7365.
 XX
 XX New G-protein coupled receptor polypeptides and polynucleotides useful
 PT for identifying compounds for treating a TGR-associated disorder, e.g.
 PT psoriasis, inflammatory bowel disease, hyperlipidemia, Parkinson's
 PT disease, anemia.
 XX
 PS Example 1; Page 64; 87pp; English.
 XX
 CC The invention relates to G-protein coupled receptor (GPCR) polypeptides
 CC and encoding polynucleotides selected from TGR20, TGR35, TGR36, TGR18,
 CC TGR341, TGR216 and TGR79. The polypeptides and nucleic acids are
 CC useful for identifying compounds for treating a TGR-associated disorder,
 CC such as psoriasis, inflammatory bowel disease, hyperlipidemia,
 CC Parkinson's disease, Huntington's disease, anemia, immune and blood
 CC disorders, ulcerative colitis. Crohn's disease or spleen enlargement.
 CC They are also useful for identifying cells such as kidney, liver,
 CC hypothalamus, colon, adipose, or spleen cells, for forensics and
 CC paternity determination, diagnosing diseases and examining signal
 CC transduction. The present sequence represents a human TGR35 polypeptide
 XX
 SQ Sequence 396 AA;

Query Match 100.0%; Score 2041; DB 6; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1e-200;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSVGVVAVTGTGVTGNVLTLLALAIQPKLRTFNLLIA 60
 DB 1 MNSSDANFSCYHESVLGYRYVAVSVGVVAVTGTGVTGNVLTLLALAIQPKLRTFNLLIA 60

QY 61 NLTLADLLYCTLLQPFVSDTYLHLHWRGTATFCRVFGLLLFASNSVSLTLCIALGRYL 120
 DB 61 NLTLADLLYCTLLQPFVSDTYLHLHWRGTATFCRVFGLLLFASNSVSLTLCIALGRYL 120

QY 121 LIAHPKLPQVFSAGKIVLALVSTVWGVASFAPLWPIYILVPVCTCFDRIRGRPYTT 180
 DB 121 LIAHPKLPQVFSAGKIVLALVSTVWGVASFAPLWPIYILVPVCTCFDRIRGRPYTT 180

QY 181 ILMGYFVLGLSSVGIFYCLIHQVRAAQAALDOYKLRQASIHNSHVARTDEAMPGRFOE 240
 DB 181 ILMGYFVLGLSSVGIFYCLIHQVRAAQAALDOYKLRQASIHNSHVARTDEAMPGRFOE 240

QY 241 LDSRLASGGPSEGISSEPVSAATTOTLEGDSSEVDQINSKRAKQMAEKSPPEASAKAQP 300
 DB 241 LDSRLASGGPSEGISSEPVSAATTOTLEGDSSEVDQINSKRAKQMAEKSPPEASAKAQP 300

QY 301 IKGARRAPDSSSEFGKVTMCMFAVFLCFALSYIPFLLNILDARVOAPRVVHMLAANLTW 360
 DB 301 IKGARRAPDSSSEFGKVTMCMFAVFLCFALSYIPFLLNILDARVOAPRVVHMLAANLTW 360

QY 361 LNCGINPVLVYAMNRQFQAYGSILKRGPRSFHRLH 396
 DB 361 LNCGINPVLVYAMNRQFQAYGSILKRGPRSFHRLH 396

RESULT 8
 ABR62422
 ID ABR62422 standard; protein; 396 AA.
 XX
 AC ABR62422;
 XX
 DT 03-OCT-2003 (first entry)
 XX
 DE Human hpl5a orphan G-protein coupled receptor.

XX Human; hp15a; receptor; G-protein coupled receptor; cardiant;
 KW gastrointestinal.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 3 /note= "potential N-glycosylation site"
 FT Modified-site 8 /note= "potential N-glycosylation site"
 FT Domain 20..46
 FT Domain /note= "Transmembrane domain 1"
 FT Domain 57..79
 FT Domain /note= "Transmembrane domain 2"
 FT Domain 95..116
 FT Domain /note= "Transmembrane domain 3"
 FT Domain 137..158
 FT Domain /note= "Transmembrane domain 4"
 FT Domain 183..205
 FT Domain /note= "Transmembrane domain 5"
 FT Domain 315..338
 FT Domain /note= "Transmembrane domain 6"
 FT Domain 351..373
 FT Domain /note= "Transmembrane domain 7"

XX WO2003054540-A1.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-US040612.

XX 19-DEC-2001; 2001US-00029436.

XX (SYNA-) SYNAPTIC PHARM CORP.

XX Smith KE, Weinschank R;

XX WPI; 2003-559173/52.

XX N-PSDB; ACC84331.

XX New recombinant nucleic acid, useful for preparing a composition for
 treating disorders linked to human hp15a receptor e.g. cardiovascular or
 gastrointestinal disorders.

XX Disclosure; Fig 2A-C; 98pp; English.

XX The present sequence is the protein sequence of a novel human orphan G-
 protein coupled receptor, designated hp15a. The endogenous ligand for
 hp15a is likely to be a neuromodulator since the receptor is present in
 several regions of the human brain. The invention provides hp15a nucleic
 acids, vectors, host cells, antibodies, probes, antisense
 oligonucleotides, transgenic non-human animals, methods of isolating the
 receptor, methods of treating an abnormality that is associated with
 activity of hp15a e.g. cardiovascular or gastrointestinal disorders, and
 methods of determining binding of compounds to hp15a

XX Sequence 396 AA;

Query Match 100.0%; Score 2041; DB 6; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1e-200;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSGVAVTGTGVNLTLLALAIQPKLRTFNLLIA 60

DB 1 MNSSDANFSCYHESVLGYRYVAVSGVAVTGTGVNLTLLALAIQPKLRTFNLLIA 60

QY 61 NLTLADLLYCTLQPPSVDTYTLHLHRTGATFCRVFGLLLFASNSVSIITLCLIALGRYL 120

DB 61 NLTLADLLYCTLQPPSVDTYTLHLHRTGATFCRVFGLLLFASNSVSIITLCLIALGRYL 120

QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVSAPLPIVILPVVCTCSFDRIRGPPYTT 180

DB 121 LIAHPKLPQVFSAGKIVLALVSTWVGVSAPLPIVILPVVCTCSFDRIRGPPYTT 180
 QY 181 ILMGIFYVLGLSSVGIFYCLIHROVKRAAQLDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
 DB 181 ILMGIFYVLGLSSVGIFYCLIHROVKRAAQLDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
 QY 241 LDSRLASGGPSEGISSEPVSAATTOTLEGDSSEVGDQINSKRAKOMAEKSPPEASAKAQP 300
 DB 241 LDSRLASGGPSEGISSEPVSAATTOTLEGDSSEVGDQINSKRAKOMAEKSPPEASAKAQP 300
 QY 301 IKGARRAPDSSSEFGKVTMCFVFLCPALSYIPFLLNLILDARVQAPRVVHMLAANLTW 360
 DB 301 IKGARRAPDSSSEFGKVTMCFVFLCPALSYIPFLLNLILDARVQAPRVVHMLAANLTW 360
 QY 361 LNCINPVLVYAAAMNQFRQAYGSILKRGPRSFHRLH 396
 DB 361 LNCINPVLVYAAAMNQFRQAYGSILKRGPRSFHRLH 396

RESULT 9

AAM99936

ID AAM99936 standard; protein; 404 AA.

XX AC AAM99936;

XX 04-JAN-2002 (first entry)

XX Human expressed polypeptide SEQ ID NO 60.

XX Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
 immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
 antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
 antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX Homo sapiens.

XX WO200155387-A1.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001310.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205151P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218230P.

XX 26-JUL-2000; 2000US-0220963P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 22-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 03-SEP-2000; 2000US-0229509P.
PR 03-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 14-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 21-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 25-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465573/50.
XX N-PSDB; AA199548.
XX
XX Isolated digestive system associated polypeptide for treating, preventing
XX and/or prognosing disorders related to the digestive system including
XX digestive system cancers and also for testing and detection e.g.
XX diagnosis.
XX
XX Claim 11; SEQ ID NO 60; 509pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AA199548-AA199604) and proteins
XX (AA199936-AA199984) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
XX breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX cardiovascular disorders such as myocardial ischaemia; (d) wound healing
XX ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX infectious diseases such as viral, bacterial, fungal and parasitic
XX infections. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 404 AA;
XX
XX Query Match 100.0%; Score 2041; DB 4; Length 404;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-200;
XX Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALALQPKLRTRFNLLIA 60
 CC 9 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALALQPKLRTRFNLLIA 68
 CC 61 NLTADLLCYCTLLQPFSSVDVTLHLHWRGTGATFCRVFGLLLFASNSVILCLIALGRYL 120
 CC 69 NLTADLLCYCTLLQPFSSVDVTLHLHWRGTGATFCRVFGLLLFASNSVILCLIALGRYL 128
 CC 121 LIAHPKLPQVFSAGIVLALVSTWVGVASFAPLWPIYILVPCVCTCFDRIRGRPYTT 180
 CC 129 LIAHPKLPQVFSAGIVLALVSTWVGVASFAPLWPIYILVPCVCTCFDRIRGRPYTT 188
 CC 181 ILMGIFYVLGLSSVGIIFYCLIHQVKRAAALDQYKLRQASIHSHVARTDEAMPGRFOE 240
 CC 189 ILMGIFYVLGLSSVGIIFYCLIHQVKRAAALDQYKLRQASIHSHVARTDEAMPGRFOE 248
 CC 241 LDSRLASGPGSEGISSEPVSAATTQTLEGDSSSEVDQINSKRAKQMAEKSPPEASAKAQP 300
 CC 249 LDSRLASGPGSEGISSEPVSAATTQTLEGDSSSEVDQINSKRAKQMAEKSPPEASAKAQP 308
 CC 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIIPFLNILDARVQAPRVVHMLAANLTW 360
 CC 309 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIIPFLNILDARVQAPRVVHMLAANLTW 368
 CC 361 LNCINPVLVYAAAMNRFQRAYGSIILKRGPRSFHRLH 396
 CC 369 LNCINPVLVYAAAMNRFQRAYGSIILKRGPRSFHRLH 404

RESULT 10
 ABB82509
 ID ABB82509 standard; protein; 396 AA.
 XX
 AC ABB82509;
 XX
 DT 22-JAN-2003 (first entry)
 XX
 DE Mouse TGR35 polypeptide.
 XX
 KW G-protein coupled receptor; GPCR; antipsoriatic; antiinflammatory;
 KW antilipemic; nootropic; neuroprotective; antianemic; antiulcer; mouse;
 KW antiparkinsonian; antilipemic; TGR35; receptor.
 XX
 OS Mus sp.
 XX
 PN WO200277001-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 08-MAR-2002; 2002WO-US007171.
 XX
 PR 09-MAR-2001; 2001US-00802803.
 PR 16-MAR-2001; 2001US-0276649P.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Tian H, Zhao J, Chen J, Cutler G;
 XX
 DR WPI; 2003-018881/01.
 DR N-PSDB; ABV73374.
 XX
 XX New G-protein coupled receptor polypeptides and polynucleotides useful
 XX for identifying compounds for treating a TGR-associated disorder, e.g.
 XX psoriasis, inflammatory bowel disease, hyperlipidemia, Parkinson's
 XX disease, anemia.
 XX
 PS Claim 53; Page 71; 87pp; English.
 XX
 CC The invention relates to G-protein coupled receptor (GPCR) polypeptides
 CC and encoding polynucleotides selected from TGR20, TGR35, TGR36, TGR183,
 CC TGR341, TGR211, TGR216 and TGR79. The polypeptides and nucleic acids are
 CC useful for identifying compounds for treating a TGR-associated disorder,

CC such as psoriasis, inflammatory bowel disease, hyperlipidemia,
 CC Parkinson's disease, Huntington's disease, anemia, immune and blood
 CC disorders, ulcerative colitis, Crohn's disease or spleen enlargement.
 CC They are also useful for identifying cells such as kidney, liver,
 CC hypothalamus, colon, adipose, or spleen cells, for forensics and
 CC paternity determination, diagnosing diseases and examining signal
 CC transduction. The present sequence represents a mouse TGR35 polypeptide
 XX
 XX Sequence 396 AA;
 Query Match 85.6%; Score 1748; DB 6; Length 396;
 Best Local Similarity 85.4%; Pred. No. 1.4e-170; Indels 0; Gaps 0;
 Matches 338; Conservative 20; Mismatches 38;
 QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALALQPKLRTRFNLLIA 60
 DB 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALALQPKLRTRFNLLIA 60
 QY 61 NLTADLLCYCTLLQPFSSVDVTLHLHWRGTGATFCRVFGLLLFASNSVILCLIALGRYL 120
 DB 61 NLTADLLCYCTLLQPFSSVDVTLHLHWRGTGATFCRVFGLLLFASNSVILCLIALGRYL 120
 QY 121 LIAHPKLPQVFSAGIVLALVSTWVGVASFAPLWPIYILVPCVCTCFDRIRGRPYTT 180
 DB 121 LIAHPKLPQVFSAGIVLALVSTWVGVASFAPLWPIYILVPCVCTCFDRIRGRPYTT 180
 QY 181 ILMGIFYVLGLSSVGIIFYCLIHQVKRAAALDQYKLRQASIHSHVARTDEAMPGRFOE 240
 DB 181 ILMGIFYVLGLSSVGIIFYCLIHQVKRAAALDQYKLRQASIHSHVARTDEAMPGRFOE 240
 QY 241 LDSRLASGPGSEGISSEPVSAATTQTLEGDSSSEVDQINSKRAKQMAEKSPPEASAKAQP 300
 DB 241 LDSRLASGPGSEGISSEPVSAATTQTLEGDSSSEVDQINSKRAKQMAEKSPPEASAKAQP 300
 QY 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIIPFLNILDARVQAPRVVHMLAANLTW 360
 DB 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIIPFLNILDARVQAPRVVHMLAANLTW 360
 QY 361 LNCINPVLVYAAAMNRFQRAYGSIILKRGPRSFHRLH 396
 DB 361 LNCINPVLVYAAAMNRFQRAYGSIILKRGPRSFHRLH 396
 RESULT 11
 AAM87595
 ID AAM87595 standard; protein; 115 AA.
 XX
 AC AAM87595;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen SEQ ID NO:15188.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001354.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
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PR 20-OCT-2000; 2000US-0240960P.
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PR 17-NOV-2000; 2000US-0249265P.
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PR 05-DEC-2000; 2000US-0256719P.
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PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251859P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX N-PSDB; AAK60376.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
PS Claim 11; SEQ ID NO 15188; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased

CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 115 AA;

Query Match 27.9%; Score 570; DB 4; Length 115;
 Best Local Similarity 99.1%; Pred. No. 2.9e-50;
 Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 213 DOYKLRQASTHSNHVARTDEAMPGRFOELDSRLASGSPSEGISSEPVSAATTOTLEGDSS 272
 DB 1 DOYKLRQASTHSNHVARTDEAMPGRFOELDSRLASGSPSEGISSEPVSAATTOTLEGDSS 60
 QY 273 EVGQINSKAKQWAEKSPPEASAKAQPICKGARRAPDSSEFGKVRMCFVAVFLC 327
 DB 61 EVGQINSKAKQWAEKSPPEASAKAQPICKGARRAPDSSEFGKVRMCFVAVFLC 115

RESULT 12
 ABB89377
 ID ABB89377 standard; protein; 124 AA.
 XX
 AC ABB89377;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 1753.
 XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200190304-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US016450.
 XX
 PR 19-MAY-2000; 2000US-0205515P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-122018/16.
 DR N-PSDB; ABL89786.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 1753; 2081pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 124 AA;

Query Match 27.8%; Score 568; DB 5; Length 124;
 Best Local Similarity 98.2%; Pred. No. 5.2e-50;
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAATGTVGNVLTLLALATQPKLRTRENLIIA 60
 DB 1 MNSSDANFSCYHESVLGYRYVAVSWGVAATGTVGNVLTLLALATQPKLRTRENLIIA 60
 QY 61 NLTLADLLYCTLLQPPFSVDYTLHLHWRGTGATFCRVFGLLLFASNSVSLTLC 112
 DB 61 NLTLADLLYCTLLQPPFSVDYTLHLHWRGTGATFCRVFGLLLFASNSVSLTLC 112

RESULT 13
 AAU18097
 ID AAU18097 standard; protein; 116 AA.
 XX
 AC AAU18097;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Novel human uterine motility-association polypeptide #4.
 XX
 KW Human; uterine motility-association disorder; uterus; pregnancy; labour;
 KW menstrual cycle; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155201-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001317.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0196350P.
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 PR 18-APR-2000; 2000US-0198123P.
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 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
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 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-02559678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 PI WPI; 2001-488777/53.
 DR N-PSDB; AAS28939.
 XX
 XX New nucleic acid molecules encoding 49 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives.
 XX
 PS Claim 11; SEQ ID NO 73; 524pp; English.
 XX
 CC The present invention relates to the isolation of novel human uterine
 CC motility-association polypeptides, and cDNA (AAS28936-AAS28994) and
 CC genomic sequences encoding for these polypeptides. The sequences of the
 CC invention are useful in the diagnosis, treatment, prevention and/or
 CC prognosis of diseases associated with uterine motility such as pregnancy
 CC and labour, and menstrual disorders. The polynucleotide sequences of the
 CC invention are also useful in gene therapy. AAU18094-AAU18152 represent
 CC human uterine motility-association polypeptides. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 116 AA;

Query Match 22.2%; Score 454; DB 4; Length 116;
 Best Local Similarity 98.9%; Pred. No. 2.5e-38;
 Matches 87; Conservative 1; Mismatches 0; Gaps 0;
 QY 1 MNSSDANFSCYHESVLGCRYVAVSWGVTGVTGNVLTLLALATQPKLRTFNLLIA 60
 DB 9 MNSSDANFSCYHESVLGCRYVAVSWGVTGVTGNVLTLLALATQPKLRTFNLLIA 68

Oy 61 NLTADLLCYTLLOPFSVDYVHLHWRT 88
 Db 69 NLTADLLCYTLLOPFSVDYVHLHWRT 96

RESULT 14
 AAUI8646
 ID AAUI8646 standard; protein; 116 AA.
 AC AAUI8646;
 XX
 DT 21-NOV-2001 (first entry)
 XX Renal and cardiovascular-associated protein, Seq ID 85.
 DE Human; antiinflammatory; neuroprotective; immunomodulator; vulnery;
 XX cardiovascular; cyrostatic; nephrotropic; antianemic; nephritis;
 KW immunosuppressive; kidney disorder; renal failure; hypertension;
 KW cardiovascular disorder; myocardial infarction; blood disorder; anaemia;
 KW blood coagulation disorder; electrolyte imbalance disorder; cancer;
 KW hyponatremia; hyperkalaemia; neoplastic disorder; nephroma;
 KW autoimmune disease; inflammatory disease; reproductive system disorder;
 KW endocrine disorder; neural activity; neurological disorder;
 KW wound healing; respiratory disorder.
 XX
 OS Homo sapiens.
 XX
 PN WC20015328-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001359.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205151P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
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Run on: September 24, 2004, 08:39:32 ; Search time 413 Seconds

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2041	100.0	396	9	US-09-798-710-2
3	2041	100.0	396	12	US-10-343-650A-46
4	2041	100.0	396	14	US-10-094-417-4
5	2041	100.0	396	14	US-10-225-567A-585
6	2041	100.0	396	14	US-10-029-436-2
7	2041	100.0	404	14	US-10-073-885-60
8	1748	85.6	396	14	US-10-094-417-22
9	1168	57.2	310	14	US-10-017-161-1922
10	568	27.8	124	15	US-10-264-237-1753
11	454	22.2	116	9	US-09-764-853-482
12	454	22.2	116	10	US-09-989-442-85
13	454	22.2	116	10	US-09-764-886-60
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17	454	22.2	116	14	US-10-073-865-73	Sequence 73, Appl
18	454	22.2	116	14	US-10-103-313-310	Sequence 310, Appl
19	454	22.2	116	14	US-10-073-883-87	Sequence 87, Appl
20	338	16.6	386	14	US-10-270-333-18	Sequence 18, Appl
21	290.5	14.2	515	14	US-10-238-129-10	Sequence 10, Appl
22	290.5	14.2	515	14	US-10-238-667-10	Sequence 10, Appl
23	290	14.2	443	14	US-10-060-795B-11	Sequence 11, Appl
24	290	14.2	443	14	US-10-157-031-78	Sequence 78, Appl
25	290	14.2	443	14	US-10-352-567A-102	Sequence 102, Appl
26	290	14.2	443	15	US-10-352-684A-2	Sequence 2, Appl
27	290	14.2	443	15	US-10-292-798-658	Sequence 558, Appl
28	288.5	14.1	466	10	US-09-992-238-19	Sequence 19, Appl
29	288.5	14.1	466	15	US-10-436-715-45	Sequence 45, Appl
30	288.5	14.1	497	13	US-10-052-589-2	Sequence 2, Appl
31	287.5	14.1	515	14	US-10-238-129-9	Sequence 9, Appl
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33	286.5	14.0	517	9	US-09-351-622-10	Sequence 10, Appl
34	286.5	14.0	517	14	US-10-325-930-10	Sequence 10, Appl
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36	285.5	14.0	520	14	US-10-185-991-4	Sequence 4, Appl
37	285.5	14.0	520	14	US-10-238-129-4	Sequence 4, Appl
38	285.5	14.0	520	14	US-10-238-667-4	Sequence 36, Appl
39	285.5	14.0	520	14	US-10-225-567A-36	Sequence 489, Appl
40	285	14.0	443	11	US-09-826-509-489	Sequence 754, Appl
41	283.5	13.9	462	14	US-10-017-161-754	Sequence 2, Appl
42	283.5	13.9	515	14	US-10-054-616A-2	Sequence 4, Appl
43	283.5	13.9	515	14	US-10-054-616A-4	Sequence 4, Appl
44	283.5	13.9	515	14	US-10-054-616A-5	Sequence 5, Appl
45	283.5	13.9	515	16	US-10-633-438-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1

US-09-826-508-38

; Sequence 38, Application US/09826508

; Patent No. US2001002509A1

; GENERAL INFORMATION:

; APPLICANT: Nabii Elshourbagy

; APPLICANT: Lisa Vawter

; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides

; TITLE OF INVENTION: and Polynucleotides

; FILE REFERENCE: GP-70744USB

; CURRENT APPLICATION NUMBER: US/09/826,508

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 38

; LENGTH: 396

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-826-508-38

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Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-798-710-2
; Sequence 2, Application US/09798710
; Publication No. US20020187947A1
; GENERAL INFORMATION:
; APPLICANT: Jatai, Gabor
; APPLICANT: Cooper, Paul Roy
; APPLICANT: Yousefi, Shida
; TITLE OF INVENTION: No. US20020187947A1e1 Gene
; FILE REFERENCE: 4-31328A/H026
; CURRENT APPLICATION NUMBER: US/09/798, 710
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/XXX,XXX
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-710-2

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Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 46, Application US/10343650A

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; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
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; SEQ ID NO 46
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-46

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RESULT 4

US-10-094-417-4
; Sequence 4, Application US/10094417
; Publication No. US20030045685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030045685A1e1 Receptors
; FILE REFERENCE: 018781-008110US
; CURRENT APPLICATION NUMBER: US/10/094,417
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/802,803
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/276,649
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

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; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
; US-10-094-417-4

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DB 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGQINSKRAKQMAEKSPPEASAKAQP 300
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DB 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396

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US-10-225-567A-585
; Sequence 585, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 585
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-585

Query Match      100.0%; Score 2041; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
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DB 61 NLTADLLYCTLLQPFSDVTYLLHLHWRGTGATFCRVFGLLLFASNSVSIITLCLIALGRYL 120
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DB 181 ILMGIVFVLGLSSVGIYFYLHROVKRAAALDOYKLRQASIHSHNHVARTDEAMPGRFOE 240
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DB 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIPFLLNILDARVQAPRVVHMLAANLTW 360
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DB 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396

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DB 61 NLTADLLYCTLLQPFSDVTYLLHLHWRGTGATFCRVFGLLLFASNSVSIITLCLIALGRYL 120
QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCFDRIIRGRPYTT 180
DB 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCFDRIIRGRPYTT 180
QY 181 ILMGIVFVLGLSSVGIYFYLHROVKRAAALDOYKLRQASIHSHNHVARTDEAMPGRFOE 240
DB 181 ILMGIVFVLGLSSVGIYFYLHROVKRAAALDOYKLRQASIHSHNHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGQINSKRAKQMAEKSPPEASAKAQP 300
DB 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIPFLLNILDARVQAPRVVHMLAANLTW 360
DB 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIPFLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
DB 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 6
US-10-029-436-2
; Sequence 2, Application US/10029436
; Publication No. US20030124138A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Weinstank, Richard L.
; TITLE OF INVENTION: DNA Encoding A Human Receptor (hpl5a) And Uses
; FILE REFERENCE: 551.80
; CURRENT APPLICATION NUMBER: US/10/029,436
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US/09/179,798A
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-029-436-2

Query Match      100.0%; Score 2041; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAATGTGNNVLTLLALAIQPKLRTFRNLLIA 60
DB 1 MNSSDANFSCYHESVLGYRYVAVSWGVAATGTGNNVLTLLALAIQPKLRTFRNLLIA 60
QY 61 NLTADLLYCTLLQPFSDVTYLLHLHWRGTGATFCRVFGLLLFASNSVSIITLCLIALGRYL 120
DB 61 NLTADLLYCTLLQPFSDVTYLLHLHWRGTGATFCRVFGLLLFASNSVSIITLCLIALGRYL 120
QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCFDRIIRGRPYTT 180
DB 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCFDRIIRGRPYTT 180
QY 181 ILMGIVFVLGLSSVGIYFYLHROVKRAAALDOYKLRQASIHSHNHVARTDEAMPGRFOE 240
DB 181 ILMGIVFVLGLSSVGIYFYLHROVKRAAALDOYKLRQASIHSHNHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGQINSKRAKQMAEKSPPEASAKAQP 300
DB 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIPFLLNILDARVQAPRVVHMLAANLTW 360
DB 301 IKGARRAPDSSSEFGKVTMCFVFLCFALSYIPFLLNILDARVQAPRVVHMLAANLTW 360

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QY 361 LNCINPVLVYAMNRQFRQAYGSLKRGPSFHLH 396
 Db 361 LNCINPVLVYAMNRQFRQAYGSLKRGPSFHLH 396

RESULT 7

US-10-073-885-60
 ; Sequence 60, Application US/10073885
 ; Publication No. US20030096346A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P0203C1
 ; CURRENT APPLICATION NUMBER: US/10/073,885
 ; CURRENT FILING DATE: 2002-02-14
 ; Prior Application removed - See file Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 60
 ; LENGTH: 404
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (7)_feature
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-10-073-885-60

Query Match 100.0%; Score 2041; DB 14; Length 404;
 Best Local Similarity 100.0%; Pred. No. 1.5e-187;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVVAVTGVNVLTLALAIQPKLRTFNLIA 60
 Db 9 MNSSDANFSCYHESVLGYRYVAVSWGVVAVTGVNVLTLALAIQPKLRTFNLIA 68
 QY 61 NLTADLLYCTLLQPFSDVTLHLHWTGATFCRVFGLLLFASNSVSLTCLIALGRYL 120
 Db 69 NLTADLLYCTLLQPFSDVTLHLHWTGATFCRVFGLLLFASNSVSLTCLIALGRYL 128
 QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
 Db 129 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 188
 QY 181 ILMGIFYVLGLSSVGIYFCLIHQVKRAAALDOYKLRQASIHSHNHVARTDEAMPGRFOE 240
 Db 189 ILMGIFYVLGLSSVGIYFCLIHQVKRAAALDOYKLRQASIHSHNHVARTDEAMPGRFOE 248
 QY 241 LDSRLASGGPSEGISSEPVSAATTTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 Db 249 LDSRLASGGPSEGISSEPVSAATTTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 308
 QY 301 IKGARRAPDSSSEFGKTRMCFVFLCFALSYIPFLNLILDARVQAPRVVHMLAANLTW 360
 Db 309 IKGARRAPDSSSEFGKTRMCFVFLCFALSYIPFLNLILDARVQAPRVVHMLAANLTW 368
 QY 361 LNCINPVLVYAMNRQFRQAYGSLKRGPSFHLH 396
 Db 369 LNCINPVLVYAMNRQFRQAYGSLKRGPSFHLH 404

RESULT 8

US-10-094-417-22
 ; Sequence 22, Application US/10094417
 ; Publication No. US20030045685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tian, Hui
 ; APPLICANT: Zhao, Jiaqiang
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: No. US20030045685A1e1 Receptors
 ; FILE REFERENCE: 018781-008110US

; CURRENT APPLICATION NUMBER: US/10/094,417
 ; CURRENT FILING DATE: 2002-06-10
 ; PRIOR APPLICATION NUMBER: US 09/802,803
 ; PRIOR FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: US 60/276,649
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 396
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) TGR35
 US-10-094-417-22

Query Match 85.6%; Score 1748; DB 14; Length 396;
 Best Local Similarity 85.4%; Pred. No. 2.4e-159;
 Matches 338; Conservative 20; Mismatches 38; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVVAVTGVNVLTLALAIQPKLRTFNLIA 60
 Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVVAVTGVNVLTLALAIQPKLRTFNLIA 60
 QY 61 NLTADLLYCTLLQPFSDVTLHLHWTGATFCRVFGLLLFASNSVSLTCLIALGRYL 120
 Db 61 NLTADLLYCTLLQPFSDVTLHLHWTGATFCRVFGLLLFASNSVSLTCLIALGRYL 120
 QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
 Db 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
 QY 181 ILMGIFYVLGLSSVGIYFCLIHQVKRAAALDOYKLRQASIHSHNHVARTDEAMPGRFOE 240
 Db 181 ILMGIFYVLGLSSVGIYFCLIHQVKRAAALDOYKLRQASIHSHNHVARTDEAMPGRFOE 240
 QY 241 LDSRLASGGPSEGISSEPVSAATTTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 Db 241 LDSRLASGGPSEGISSEPVSAATTTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
 QY 301 IKGARRAPDSSSEFGKTRMCFVFLCFALSYIPFLNLILDARVQAPRVVHMLAANLTW 360
 Db 301 IKGARRAPDSSSEFGKTRMCFVFLCFALSYIPFLNLILDARVQAPRVVHMLAANLTW 360
 QY 361 LNCINPVLVYAMNRQFRQAYGSLKRGPSFHLH 396
 Db 361 LNCINPVLVYAMNRQFRQAYGSLKRGPSFHLH 396

RESULT 9

US-10-017-161-1922
 ; Sequence 1922, Application US/10017161
 ; Publication No. US20030143688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUWA, MAKIRO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: ABURATANI, HIROYUKI
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/0152
 ; CURRENT APPLICATION NUMBER: US/10/017,161
 ; CURRENT FILING DATE: 2002-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001/246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 2430
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1922
 ; LENGTH: 310
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (20)..
 (53)

OTHER INFORMATION: Variable amino acid
 FEATURE:
 NAME/KEY: MOD RES
 LOCATION: (66)
 OTHER INFORMATION: Variable amino acid
 FEATURE:
 NAME/KEY: MOD RES
 LOCATION: (289)
 OTHER INFORMATION: Variable amino acid
 US-10-017-161-1922

Query Match 57.2%; Score 1168; DB 14; Length 310;
 Best Local Similarity 94.2%; Pred. No. 1.2e-103;
 Matches 226; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
 QY 153 APLWPIYILPVVCTCSFDRIGRPYTTILMGIYFVLGLSSVGIYCLIHROVKGAQAAL 212
 DB 70 APLWPIYILPVVCTCRWDRIQSRPYTTILMGIYFVLGLSSVGIYCLIHROVKGAQAAL 129
 QY 213 DQYKLRQASIHNVHARTDEMPGRFOELDSRLASGGPSEGISBPVSAATTQTLEGDS 272
 DB 130 DQYKLRQASIHNVHARTDEMPGRFOELDSRLASGGPSEGISBPVSAATTQTLEGDS 189
 QY 273 EVGDQINSKRAKQMAEKSPPEASAKAQPIKGARRAPDSSSEFGKVTMCFVFLCFALSY 332
 DB 190 EVGDQINSKRAKQMAEKSPPEASAKAQPIKGARRAPDSSSEFGKVTMCFVFLCFALSY 249
 QY 333 IPELLIILIDARVOAPRVVHMLAANLTWLCINPVLVYAMNRQPRQAVGSLKGRPSF 392
 DB 250 IPELLIILIDARVOAPRVVHMLAANLTWLCINPVLVYAMNRQPRQAVGSLKGRPSF 309

RESULT 10
 US-10-264-237-1753
 ; Sequence 1753, Application US/10264237
 ; Publication No. US20040009491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA131P1
 ; CURRENT APPLICATION NUMBER: US/10/264,237
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/16450
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: US 60/205,515
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 2876
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 1753
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (85)_FEATURE
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (97)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 US-10-264-237-1753

Query Match 27.8%; Score 568; DB 15; Length 124;
 Best Local Similarity 98.2%; Pred. No. 1.8e-46;
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MNSSDANFSCYHESVILGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRLNLLIA 60
 DB 1 MNSSDANFSCYHESVILGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRLNLLIA 60
 QY 61 NLTADLLYCTLLQPFVSDTYLHLHWTGATFCRVFGLLLFASNSVSLTLC 112
 DB 61 NLTADLLYCTLLQPFVSDTYLHLHWTGATFCRVFGLLLFASNSVSLTLC 112

RESULT 11
 US-09-764-853-482
 ; Sequence 482, Application US/09764853
 ; Patent No. US20020090672A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P0206
 ; CURRENT APPLICATION NUMBER: US/09/764,853
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 939
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 482
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (7)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (93)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (104)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-764-853-482

Query Match 22.2%; Score 454; DB 9; Length 116;
 Best Local Similarity 98.9%; Pred. No. 1.5e-35;
 Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNSSDANFSCYHESVILGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRLNLLIA 60
 DB 9 MNSSDANFSCYHESVILGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRLNLLIA 68
 QY 61 NLTADLLYCTLLQPFVSDTYLHLHWT 89
 DB 69 NLTADLLYCTLLQPFVSDTYLHLXWRT 96

RESULT 12
 US-09-989-442-85
 ; Sequence 85, Application US/09989442
 ; Publication No. US20030013649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P0208
 ; CURRENT APPLICATION NUMBER: US/09/989,442
 ; CURRENT FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 60/179,065
 ; PRIOR FILING DATE: 2000-01-31
 ; PRIOR APPLICATION NUMBER: 60/180,628
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: 60/214,886
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/217,487
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,758
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,963
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/217,496
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,447
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/218,290
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/225,757

; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/226,868
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/216,647
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,267
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/216,880
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,270
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/251,869
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/235,834
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/234,274
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/234,223
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/228,924
 ; PRIOR FILING DATE: 2000-08-30
 ; PRIOR APPLICATION NUMBER: 60/224,518
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/236,369
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/224,519
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,964
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/241,809
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/249,299
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/236,327
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/241,785
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/244,617
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 60/225,268
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/236,368
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/251,856
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/251,868
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/229,344
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/234,997
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: 60/229,343
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,345
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,287
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,513
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/231,413
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/229,509
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/236,367
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/237,039
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,038
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/236,370
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/236,802
 ; PRIOR FILING DATE: 2000-10-02

; PRIOR APPLICATION NUMBER: 60/237,037
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,040
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/240,960
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/239,935
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/239,937
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/241,787
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/246,474
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/246,532
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/249,216
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,210
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/226,681
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,759
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/225,213
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/227,182
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,214
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/235,836
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/230,438
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/215,135
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: 60/225,266
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 ; PRIOR APPLICATION NUMBER: 60/249,218
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 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,213
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,212
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,207
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,245
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,244
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,217
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,211
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,215
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,264
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,214
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,297
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/232,400
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 60/231,242
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/232,081
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/232,080
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/231,414

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; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match 22.2%; Score 454; DB 10; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 68

QY 61 NLTLDLLYCTLLQPFSDVDTYHLHWRT 88
Db 69 NLTLDLLYCTLLQPFSDVDTYHLHWRT 96

RESULT 13
US-09-764-886-60
; Sequence 60, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; FEATURE:
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-886-60

Query Match 22.2%; Score 454; DB 10; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 68

QY 61 NLTLDLLYCTLLQPFSDVDTYHLHWRT 88
Db 69 NLTLDLLYCTLLQPFSDVDTYHLHWRT 96

RESULT 14
US-09-764-886-60
; Sequence 60, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 641
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; FEATURE:
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-886-60

Query Match 22.2%; Score 454; DB 11; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 68

QY 61 NLTLDLLYCTLLQPFSDVDTYHLHWRT 88
Db 69 NLTLDLLYCTLLQPFSDVDTYHLHWRT 96

RESULT 15
US-09-764-886-60
; Sequence 60, Application US/09764886
; Publication No. US20020086822A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; FEATURE:
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-886-60

Query Match 22.2%; Score 454; DB 10; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 68

QY 61 NLTLDLLYCTLLQPFSDVDTYHLHWRT 88
Db 69 NLTLDLLYCTLLQPFSDVDTYHLHWRT 96

RESULT 14
US-09-764-875-641
; Sequence 641, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P202
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 641
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; FEATURE:
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-875-641

Query Match 22.2%; Score 454; DB 11; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSGVAVTGVNLTLLALAIQPKLRTRENLLIA 68

QY 61 NLTLDLLYCTLLQPFSDVDTYHLHWRT 88
Db 69 NLTLDLLYCTLLQPFSDVDTYHLHWRT 96

RESULT 15
US-09-764-886-60
; Sequence 60, Application US/09764886
; Publication No. US20020086822A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; FEATURE:
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-886-60
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; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-886-60

```

```

Query Match      22.2%; Score 454; DB 12; Length 116;
Best Local Similarity 98.9%; Fred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVIGRYVAVSWGVTGVTGNVLTLLALAIQPKLRTFNLIIA 60
Db 9 MNSSDANFSCYHESVIGRYVAVSWGVTGVTGNVLTLLALAIQPKLRTFNLIIA 68

QY 61 NLTADLLYCTLLQPFSDTVLHLHRT 88
Db 69 NLTADLLYCTLLQPFSDTVLHLXRT 96

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Search completed: September 24, 2004, 08:57:02
Job time : 414 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 08:00:36 ; Search time 43 Seconds

(without alignments)
885.857 Million cell updates/sec

Title: US-10-029-436-2

Perfect score: 2041

Sequence: 1 MNSSDANPSCYHESVLGYR.....FRQAYGSILKGRPSFRLH 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	18.5	670	2 TL3739	probable hormone r
2	309	15.1	572	2 J13740	probable hormone r
3	292.5	14.3	515	2 J13740	alpha-1B-adrenergi
4	291	14.3	442	1 DYXLD2	dopamine receptor
5	290	14.2	443	1 DYHDD2	dopamine receptor
6	288.5	14.1	515	2 A40491	alpha-1-adrenergi
7	288	14.1	444	1 DYBOD2	dopamine receptor
8	286.5	14.0	517	2 A45121	alpha-1B-adrenergi
9	286.5	14.0	592	2 T25837	hypothetical prote
10	283.5	13.9	444	1 DYMSD2	dopamine receptor
11	283.5	13.9	444	1 S08146	dopamine receptor
12	281.5	13.8	466	2 A35375	alpha-1C-adrenergi
13	280	13.7	484	2 S58658	G protein-coupled
14	278.5	13.6	423	2 JC7677	allatostatin recep
15	278.5	13.6	466	2 I57959	alpha-1C-adrenergi
16	274	13.4	429	2 S65656	alpha-1C-adrenergi
17	274	13.4	466	2 JN0765	alpha-1C-adrenergi
18	274	13.4	499	2 S65657	d3 dopamine recept
19	272.5	13.4	400	2 G01977	alpha-1A adrenergi
20	272	13.3	477	2 S71323	dopamine receptor
21	270.5	13.3	511	2 G56849	alpha-1A adrenergi
22	270.5	13.3	560	2 A38731	D3 dopamine recept
23	268.5	13.2	400	2 G00013	dopamine receptor
24	267.5	13.1	446	1 DVRTD3	dopamine receptor
25	267.5	13.1	446	2 I48322	dopamine receptor
26	266	13.0	400	2 S32804	beta-3-adrenergi
27	264.5	13.0	357	2 JC7319	probable allatosta
28	261.5	12.8	458	2 A40382	alpha-2-adrenergi
29	259	12.7	365	2 A45260	serotonin receptor

ALIGNMENTS

RESULT 1

TU3739

Probable hormone receptor 22E5.11 [similarity] - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13739

R:Murphy, L.; Harris, D.; Barrell, B.

submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17668

A:Accession: T13739

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-670 <MUR>

A:Cross-references: EMBL:AL031765; NID:e1371523; PID:e1326037; PIDN:CAA21123.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0000667

A:Introns: 30/2; 77/2; 400/1

A>Note: EG:22E5.11

Query Match 18.5%; Score 378; DB 2; Length 670;

Best Local Similarity 26.4%; Pred. No. 2.5e-23;

Matches 102; Conservative 79; Mismatches 165; Indels 40; Gaps 10;

QY	7	ANFSCYHESVLGYRVAVSVGWVAVTGVGNVLTLLALAIQPKLRTFNLNLIANLTAD 66	
DB	26	ADATGFSQSLTFAAVMT---FLIMIVGICNLLTVALLKCPKVRNVAFAFISLCIAD 82	
QY	67	LLYCTLLQPFSDTYLHLHWRGTGFCRVFGLLFASNSVILTCLIALGRLYLIAHPK 126	
DB	83	LLFCALVLPFQGLRFVQGTWRHGQVLCRLIPFIQYGNIGVSLLCIAMITINRYVMITHG 142	
QY	127	LFPQVFSKGVIALVSTVWVGVSAPL---WPIYILVPVVTCS-FDRIRGRPYTI 181	
DB	143	LYARIYKRWIAVMTAACMLFSYQMQLPTLLGEWGRFGYDSRLQTCISINTDDHSSKIT 202	
QY	182	LMGIVFVLGSLSVGFYCLIHQVKRAAQALDQYKLRQASIHNSHNVARTDEAMPGRFOEL 241	
DB	203	LFITAFVPLVILAIYAKIFWVHKSQRLKSHATKQNSI-----PNNLRPL 250	
QY	242	DSRLAGSGSEGISSEPSVAATQTLEGDSSVGVQINSKAKQMAEKSPPEASAKAP- 300	
DB	251	AS-TGSGALPAGACQP-----SNRVSSDSSSFSDIVPETAP---SKQOQT 294	
QY	301	-IKGARRAPDSSSEKGVTRMCFVFLGCFALSYIPFLINILIDARVQAPRVVHMLAAMIT 359	
DB	295	RVDQREVRKKNW-RITKVLALFELFVVCYLITIVKVADKNVHPS-LHICSYILL 352	
QY	360	WLNGCINPVLVAAMNQPRQAYGSIL 385	
DB	353	YLSACINPIIYIMNKQVKAYKTVV 378	

RESULT 2

Ti3740
 probable hormone receptor 22E5.10 [similarity] - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
 C:Accession: Ti3740
 R:Murphy, L.; Harris, D.; Barrell, B.
 submitted to the EMBL Data Library, April 1999
 A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
 A:Reference number: Z17668
 A:Accession: Ti3740
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-572 <MUR>
 A:Cross-references: EMBL:AL031765; NID:e1371523; PID:e1329906; PIDN:CAA21124.1
 C:Genetics:
 A:Introns: 218/2; 426/2
 A>Note: EG:22E5.10

Query Match 15.1%; Score 309; DB 2; Length 572;
 Best Local Similarity 22.4%; Pred. No. 1.1e-17;
 Matches 102; Conservative 83; Mismatches 180; Indels 90; Gaps 10;
 QY 9 FSCYHESVGYAVSNGVVAVTGVGNVLTLLALAIQPKLRTFNLLIANLTADLL 68
 DB 100 FEGSDLLTIANWAC---IVFIIVGPNULTVALSRGQTRNSTAIINUSCDLL 156
 QY 69 YCTLLQPPSVDTYHLHWRGTGATFCRVFGLLFPASNSVILTCLIALGRYLLIAHPKLP 128
 DB 157 FGCNPLAAGTFKERAETHSDLLCRLLFPMLRYGLLAVSLLSLITINRYIIIAHPQY 216
 QY 129 PQVESAKIVLALVSTVWVGASAP---LWPIYILVPVCTCSFORIR-GRPYTILM 193
 DB 217 PRIYQRYALMVAGTWTITTSIMPTWRGVGIFGLDVSGISCMHIDRYGRSPKEFLF 276
 QY 184 GIYFVLGSSVGYFCYLIHROVKAA---LNLIDARVQAPRVVHMAANLTWLNGLNIPVYAA 219
 DB 277 IAAFMVPCICVICVARIFLLVRKAAATAGTAVTNVSDVTPSSAPQHQIQAATPKPE 336
 QY 220 ASIHSNHVARTDEAMPQFQELDSRLASGSPSEGISSEPVG----- 260
 DB 337 KVTSS--GEANEPIAGPFVVEENLAYIDDNASTDSLPSISIRRRDQDQPPVDANV 394
 QY 261 -----AATTOTLEGDSSEVDQINSKRAQMAEKSPPEA----- 294
 DB 395 VLKEREKEDRQEKVSLGRSQTQLENGKTHGKNPITTSLTTSFTFSRPSKSHYASGN 454
 QY 295 SAKAQPIKARRAPDSSEFOKVTMCFVFLCPALSYIPFLNLTIDARVQAPRVVH-- 352
 DB 455 TSNASSIYPGR---MSAKDRLLKMLIVFWFVVICYLPITVAKIWKSAE---VHPF 506
 QY 353 -MLAANLTWLNGLNIPVLYAANNRQFQVGSILK 386
 DB 507 NIAGYLLIYLTCTINPLIYVLMSEYRAYWNLRL 541

RESULT 3

JC1525
 alpha-1B-adrenergic receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999
 C:Accession: JC1525; S08400
 R:Guo, B.; Kuros, G.
 Gene 131, 243-247, 1993
 A:Title: Isolation and characterization of the gene encoding the rat alpha 1B adrenergic
 A:Reference number: JC1525; MUID:94010315; PMID:8406017
 A:Accession: JC1525
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-515 <GAO>
 A:Cross-references: GB:L08610; NID:G202624; PIDN:AAA04647.1; PID:G202626

R;Voigt, M.M.; Kispert, J.; Chin, H.
 Nucleic Acids Res. 18, 1053, 1990
 A:Title: Sequence of a rat brain cDNA encoding an alpha-1B adrenergic receptor.
 A:Reference number: S08400; MUID:90192094; PMID:2156222
 A:Accession: S08400
 A:Molecule type: mRNA
 A:Residues: 1-202, 'C', 204-206, 'C', 208-305, 'C', 307-414, 'QK', 417-439, 'C', 441-483, 'ATA', 487-
 A:Cross-references: EMBL:X51585; NID:G55557; PIDN:CAA35934.1; PID:G55558
 C:Genetics:
 A:Introns: 317/1
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 Query Match 14.3%; Score 292.5; DB 2; Length 515;
 Best Local Similarity 25.2%; Pred. No. 2.2e-16;
 Matches 97; Conservative 71; Mismatches 150; Indels 67; Gaps 12;
 QY 23 AVSWGWWVA---VTGTVGNVLTLLALAIQPKLRTFNLLIANLTADLLYCTLLQPPSV 79
 DB 45 AISVGLVIGAFILFAIVGNILVLSVACNRHLRTNFIYNLAIDALLSFTVLPFSAT 104
 QY 80 TYLHLHWRGTGATFCRVFGLLFPASNSVILTCLIALGRYLLIAHPKLPQVFSAGIVL 139
 DB 105 LEVLGYWVLGRIFCDIWAADVLCCTATSLCAISIDRYIGVYSLOYPTLVTRKAIL 164
 QY 140 ALVSTWVVG-VASAPL--WPIYILVPVCTCSFDRISGRPYTILMGI-YFVLGLSSVG 195
 DB 165 ALLSVWVLTSTVISIGPLGK---EPAPNDKCEGVTEEPFYALFSSLGSIYIPLAVIL 220
 QY 196 IFYCLIHQVKRAQAALQYKLRQASIHSHNVARTDEAMPQFQELDSRLASGSPSEGIS 255
 DB 221 VVVCVYIVAKRTTKNLEAGVWKMS-----NSKELTLRIHSKNPHE-- 262
 QY 256 SEPVSAAITOTLEGDSSEVDQINSKRAQMAEKSPPEASAKAQPIKARRAPDSSSFG 315
 DB 263 -----DTLSSTKAK---GHNPRSSIAVKLFKFSRE-KKAATLGL 297
 QY 316 KVTRMCFVFLCFALSYIPFL--LNLIDARVQAPRVVHMAANLTWLNGLNIPVYAA 372
 DB 298 IVVGM-----FILSWLPPFIAPLPLGSLFSTLKPDPDAVKVFWLGYFNSCLNPIIYPC 350
 QY 373 MNRQFQVGSILK---RGRPSFHR 394
 DB 351 SSKEFKRAFMRIILGCGCRGRRRR 375
 RESULT 4
 DYXLD2
 dopamine receptor D2 - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
 C:Accession: S14827
 R:Martens, G.J.M.; Molhuizen, H.O.F.; Groeneveld, D.; Roubos, E.W.
 FEBS Lett. 281, 85-89, 1991
 A:Title: Cloning and sequence analysis of brain cDNA encoding a Xenopus D(2) dopamine rec
 A:Reference number: S14827; MUID:91200321; PMID:1826663
 A:Accession: S14827
 A:Molecule type: mRNA
 A:Residues: 1-442 <MAR>
 A:Cross-references: EMBL:X59500; NID:G64648; PIDN:CAA42088.1; PID:G64649
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; neurotransmin
 F1:1-442/Product: dopamine receptor D2 (long form) #status predicted <Mar1>
 F1-232,266-442/Product: dopamine receptor D2 (short form) #status predicted <Mar2>
 F:32-53/Domain: transmembrane #status predicted <TM1>
 F:65-88/Domain: transmembrane #status predicted <TM2>
 F:103-124/Domain: transmembrane #status predicted <TM3>
 F:146-168/Domain: transmembrane #status predicted <TM4>
 F:182-204/Domain: transmembrane #status predicted <TM5>
 F:205-372/Domain: intracellular #status predicted <INT>
 F:373-396/Domain: transmembrane #status predicted <TM6>
 F:405-428/Domain: transmembrane #status predicted <TM7>
 F:5,15,18,169/Binding site: carbohydrate (Asn) #status predicted

F;223/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 14.3%; Score 291; DB 1; Length 442;
Best Local Similarity 24.6%; Pred. No. 2,4e-16;
Matches 111; Conservative 75; Mismatches 176; Indels 90; Gaps 13;

QY 8 NFGCYHESVLG-----YRYVAVSGVAVTGVGVNVLALLAALQPKLRTRF 55
DB 5 NLSMYNDINDNGTNGTAVDQKPHNYAMLLTLFVFI-VFGNVLVCIASREKALQTTT 63
QY 56 NLLIANUTLADLLVCTLLQPFSDVDTYLLHLHWRGTGATFCRVFGLLLFASNSVSLTLCILIA 115
DB 64 NYLIVSLAVADLLVATLVMFWAVYMEVGVGERSRTHCDIFVTLDMVMCTASILNLCALS 123
QY 116 LGRYLIAHKLPPQVFSAGKIVLAVSTVWVGASAPLWPIYILVPPVC-----T 167
DB 124 IDRYTAVAMPNLNTRYSSRRRTVMIS--VWVLGFA-----ISCPILFGLNNTGSKV 175
QY 168 CSFDRIGRPTIL-MGIYFVLGLSSGIFCYLIHQVKRA-----AQLADQV---- 215
DB 176 CIIDNPAFVYSSIVSYFVFIIVTLVYQIYVLRKRKRKRVNKNRSGVAVDAHKDC 235
QY 216 -----KLQASIHNNHVAETDEAMPGRFOELDSRLASGGPSEGISSEPVSAATT----- 264
DB 236 THPEDVKLCSFVKSGNSFPADKKVILVQE-----AGKHPDMEMEMMSSTSPPEKTK 289
QY 265 -QLEGDSSEVGQDQINSKRAKQMAEKSPPEASAKAQ----- 299
DB 290 HKASPDHNLQVATPATSNOCKNASTSPVSPYKAENKHPKDKSTPKAKVFEIQSPENKG 349
QY 300 ---PIKARAPDSSSFFGKVTMCFVFLCFALSIPFLNILDARVQAPVWHMLAA 356
DB 350 TRSITKMSKKLSQHKKEKATQMLAIVLGVFFICMLPFIILHNNHCNC-NIPQALYS 408
QY 357 NLTWL---NGCINPVLVAANNRQFRQAYGSIL 385
DB 409 AFTWLGVYNSAVNPILYITTFNVEFRKAFIKIL 440

RESULT 5

DYH02

Dopamine receptor D2 - human
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 21-Jul-2000
C/Accession: S08417; S08618; S20842; A33392; A34502; A37013; A37384; A48409; S40694
R/Robakis, N.K.; Mohamadi, M.; Fu, D.Y.; Sambamurti, K.; Refolo, L.M.
Nucleic Acids Res. 18, 1299, 1990
A/Title: Human retina D2 receptor cDNAs have multiple polyadenylation sites and differ
A/Reference number: S08417; MUID:90206805; PMID:2138729
A/Accession: S08417
A/Molecule type: mRNA
A/Residues: 1-443 <ROB>
A/Cross-references: EMBL:X51362; NID:930495; PIDN:CAA35746.1; PID:G30496
R/dal Ioso, R.; Sommer, B.; Ewert, M.; Herb, A.; Pritchett, D.B.; Bach, A.; Shivers, B.D.
EMBO J. 8, 4025-4034, 1989
A/Title: The dopamine D2 receptor: two molecular forms generated by alternative splicing
A/Reference number: S09618; MUID:90076122; PMID:2531656
A/Accession: S09618
A/Molecule type: mRNA
A/Residues: 1-443 <DL>
A/Cross-references: EMBL:X51645; NID:930867; PIDN:CAB56463.1; PID:95921480
A/Accession: S20842
A/Molecule type: DNA
A/Residues: 179-379 <DA2>
A/Cross-references: EMBL:X51646; NID:930868; PIDN:CAB37869.1; PID:94467834
R/Selbie, L.A.; Hayes, G.; Shine, J.
DNA 8, 683-689, 1989
A/Title: The major dopamine D2 receptor: molecular analysis of the human D2-A subtype.
A/Reference number: A33392; MUID:90126238; PMID:2533064
A/Accession: A33392
A/Molecule type: mRNA
A/Residues: 1-443 <SEL>
A/Cross-references: GB:M30625; NID:9181431; PIDN:AAA80024.1; PID:9181432

R/Grandy, D.K.; Marchionni, M.A.; Makam, H.; Stofko, R.E.; Alfano, M.; Frothingham, L.;
Proc. Natl. Acad. Sci. U.S.A. 86, 9762-9766, 1989
A/Title: Cloning of the cDNA and gene for a human D-2 dopamine receptor.
A/Reference number: A34502; MUID:9009344; PMID:2532362
A/Accession: A34502
A/Molecule type: mRNA
A/Residues: 1-443 <GRA>
A/Cross-references: GB:M39066; NID:9181828; PIDN:AAA52761.1; PID:9181829; GB:M77247; GB:1
R/Stoermann, T.M.; Gdula, D.C.; Weiner, D.M.; Brann, M.R.
Mol. Pharmacol. 37, 1-6, 1990
A/Title: Molecular cloning and expression of a dopamine D2 receptor from human retina.
A/Reference number: A37013; MUID:90136534; PMID:2137193
A/Accession: A37013
A/Molecule type: mRNA
A/Residues: 1-241,271-443 <STO>
R/Selbie, L.A.; Hayes, G.; Shine, J.
Adv. Second Messenger Phosphoprotein Res. 24, 9-14, 1990
A/Title: DNA homology screening: isolation and characterization of the human D2-A dopamine
A/Reference number: A37384; MUID:91000955; PMID:2144985
A/Accession: A37384
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-443 <SE2>
A/Experimental source: fetal brain and pituitary
R/Deary, A.; Palardieu, P.; Shores, C.; Caron, M.G.
Cell. Mol. Neurobiol. 11, 437-453, 1991
A/Title: D2 dopamine receptors in the human retina: cloning of cDNA and localization of
A/Reference number: A48409; MUID:92076439; PMID:1835903
A/Accession: A48409
A/Molecule type: mRNA
A/Residues: 1-241,271-443 <DEA>
A/Cross-references: GB:S69899; NID:G240290; PIDN:AAB20571.1; PID:G240291
A/Experimental source: retina
A/Note: sequence extracted from NCBI backbone (NCBIN:69899, NCBI:69900)
R/Araki, K.; Kuwano, R.; Morii, K.; Hayashi, S.; Minoshima, S.; Shimizu, N.; Katagiri, T.
Neurochem. Int. 21, 91-98, 1992
A/Title: Structure and expression of human and rat D2 dopamine receptor genes.
A/Reference number: S40694; MUID:93264902; PMID:1363862
A/Accession: S40694
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-39,271-443 <ARA>
A/Cross-references: GB:S62137; NID:G405309; PIDN:AAB26819.1; PID:G405310
C/Genetics:
A/Cross-references: GDB:119852; OMIM:126450
A/Map position: 11q23.1-11q23.1
A/Intons: 178/1; 241/3; 270/3; 380/1
C/Superfamily: vertebrate rhodopsin
C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;1-443/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-241,271-443/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;38-59/Domain: transmembrane #status predicted <TM1>
F;71-94/Domain: transmembrane #status predicted <TM2>
F;109-130/Domain: transmembrane #status predicted <TM3>
F;152-174/Domain: transmembrane #status predicted <TM4>
F;188-210/Domain: transmembrane #status predicted <TM5>
F;211-373/Domain: intracellular #status predicted <CYT>
F;374-397/Domain: transmembrane #status predicted <CYT>
F;406-429/Domain: transmembrane #status predicted <TM6>
F;517,123/Binding site: carboxylate (Asn) (covalent) #status predicted
F;107-182/Disulfide bonds: #status predicted
F;443/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 14.2%; Score 280; DB 1; Length 443;
Best Local Similarity 25.8%; Pred. No. 3e-16;
Matches 114; Conservative 65; Mismatches 183; Indels 80; Gaps 15;

QY 2 WNSSDANFSCYHESVLGRYVAVSGVAVTGVGVNVLALLAALQPKLRTRFNILLIAN 61
DB 22 FNGSGKADRPH-----YNYATLTLTLLIATV-VFGNVLVCMVAVSREKALQTTTWLVLS 75
QY 62 LTLADLLVCTLLQPFSDVDTYLLH--HWRTGATFCRVFGLLLFASNSVSLTLCIALGKY 119

Db 76 LAVADLLVATLMPVWV--YLEVGVGEWKFRIHCDIFVTLDMVMCTASILNLCAISIDRY 133
 QY 120 LLIHAPKLPQVFSKAGVLAIVSTWVGVASFAPLPIYILVPVCTCSPDRIRGRPYT 179
 Db 134 TAVAMPMLNTRYSSKRRTVMIS--IVWLVSFT-----ISCLPLFLGLNADQNE 181
 QY 180 TILMGIYFVLGLSSVGIF-----YCLIHRO-----VKRAAQAAL----- 212
 Db 182 CLIANPAFVVSSIVSFVPIVLLVYIKIYIVLRRKRVTNKRRAFRALRAPLK 241
 QY 213 -----DOYKLRQASIHNN---HVARDEAMPGRFQELD-SRLASGGSPSEGISSEPVSA 262
 Db 242 GNCNTHPEMCKLCTVIMKENGSPVNRVRAARRAQELEMELSGSTPPERTRYSPIPS 301
 QY 263 TTQLEGSSSEVG-----DOINKKRAQMAEKSPPEASAKAQPIKGARR 306
 Db 302 HHQLTLPDPSHHGLHSTPDSAPKEKNGHAKHPIKIFBIQTWPNKTRTS-LKTMRS 360
 QY 307 APDSSEFGKTRMCFVFLCFALSYIPFLNLTILDARVQAPRVVHMLAANLTWL---NG 363
 Db 361 RKLQOKEKATQMLAIVLGVFIICWLPFFTHILNIHCDG-NIPPVLYSAFTWLVYNS 419
 QY 364 CINPVLYAAMNRQROAQSIL 385
 Db 420 AVNPIIYTFNIEFRKAPLKIL 441

RESULT 6

A40491

alpha-1-adrenergic receptor - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999

C:Accession: A40491

R:Correcchia, S.; Schwinn, D.A.; Randall, R.R.; Lefkowitz, R.J.; Caron, M.G.; Kobilka, B.

Proc. Natl. Acad. Sci. U.S.A. 85, 7159-7163, 1988

A:Title: Molecular cloning and expression of the cDNA for the hamster alpha-1-adrenergic

A:Reference number: A40491; MUID:89017157; PMID:2845398

A:Accession: A40491

A:Molecule type: mRNA

A:Residues: 1-515 <COT>

A:Cross-references: GB:J04084; NID:G619407; PIDN:AAA58964.1; PID:G619408

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 14.1%; Score 288.5; DB 2; Length 515;
 Best Local Similarity 25.1%; Pred. No. 4.7e-16;
 Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY 2 WNS-SDANFSVYH-----SVLGIRYV--AVSWGIVVA---VTGTVGNVLTLLALAIQPKL 51
 Db 17 WGLKQANFTGPNCTSSNSTLPQDVTFAISVGLVGLAFILFAIVGNILVLSVACNHL 76
 QY 52 RTRFNLIANTLADLLYCTLLQPSVDVTVLHLHRTGATCFRVFGLLLFASNSVSLTL 111
 Db 77 RPTNYFTVNLAIADLLSFTLPFSATLEVLGVWLGRIPCDIWAADVLCCTASILS 136
 QY 112 CLIALGRYLLAHAPKLPQVFSKAGVLAIVSTWVGV--VASFAPL--WPIYILVPVCTC 168
 Db 137 CAISIDRIGVRYSLQPTLVTRKAILALLSVWLSTVISIGPLLGK-----EPAPND 192
 QY 169 SFDRIGRPYTILMGI--YFVLGLSSVGIYFCLIHROKRAQAALDOYKLRQASIHNNV 227
 Db 193 KECGVTEPFYALPSSLSGFIPLAVILVMYCRVIVAKRTTKLEAGVWKMS----- 246
 QY 228 ARTDEAMPGRFQELDSRLASGSPSEGISSEPVSAATTQTLEGSSSEVGDOINKKRAQMA 287
 Db 247 -----NSKEJTLRIHSKNFHE-----DTLSSTKAK--- 271
 QY 288 EKSPPEASAKAQPIKGARRAPDSSEFGKTRMCFVFLCFALSYIPFLNLTILDAR 344
 Db 272 -GHNPRSSIAVKLFKFSRE-KKAATLGIIVGM-----FILCWLPFFIALPLGSLFST 322

QY 345 VOAPRVVHMLAANLTWLNCGINPVLYAAMNRQROAQSILKRGPRSFHR 394
 Db 323 LKPPDAVFKVFWLGVFNCLNPIIYPCSSKEFKAFMRILGCQCSGR 372

RESULT 7

DYBOD2

dopamine receptor D2 - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C:Accession: S08163

R:Chio, C.L.; Hess, G.F.; Graham, R.S.; Huff, R.M.

Nature 343, 266-269, 1990

A:Title: A second molecular form of D2 dopamine receptor in rat and bovine caudate nuclei

A:Reference number: S08163; MUID:90136899; PMID:2137198

A:Accession: S08163

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-444 <CHI>

A:Cross-references: GB:X51657; NID:G304; PIDN:CAA35970.1; PID:G305

C:Superfamily: vertebrate rhodopsin

C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;

F:1-444/Product: dopamine receptor D2 (long form) #status predicted <MAT1>

F:1-241, 271-444/Product: dopamine receptor D2 (short form) #status predicted <MAT2>

F:1-94/Domain: transmembrane #status predicted <TM1>

F:109-130/Domain: transmembrane #status predicted <TM2>

F:152-174/Domain: transmembrane #status predicted <TM3>

F:188-210/Domain: transmembrane #status predicted <TM4>

F:211-374/Domain: transmembrane #status predicted <TM5>

F:375-398/Domain: transmembrane #status predicted <TM6>

F:407-430/Domain: transmembrane #status predicted <TM7>

F:5,17,23/Binding site: carboxylate (Asn) (covalent) #status predicted

F:107-182/Disulfide bonds: #status predicted

F:444/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 14.1%; Score 288; DB 1; Length 444;

Best Local Similarity 26.8%; Pred. No. 4.4e-16;

Matches 112; Conservative 65; Mismatches 181; Indels 60; Gaps 14;

QY 19 YRIVAVSGVGVAVTGTGVGNVLTLLALAIQPKLRFNLIANTLADLLYCTLLQPSV 78
 Db 34 YNYVAMLLTLFI--VFQNVLCVNAVRKALQTTNVLIVSLAVADLLVATLMPVWV 92
 QY 79 DTYLHL--HWRTGATFCRVFGLLLFASNSVSLTLCLIALGRYLLAHAPKLPQVFSAG 136
 Db 93 --YLEVGEWKFRIHCDIFVTLDMVMCTASILNLCAISIDRYTAVAMPMLNTRYSSK 150
 QY 137 IVLAIVSTWVGVASFAPLPIYILVPVCTCSPDRIRGRPYTILMGI-----YFVLG 190
 Db 151 RVTVMIA--IVWLVSFTISCP--MLFGLNNTDNECIIANPAFVVSSIVGFYVPIVTL 206
 QY 191 LSSVGIFCYLHRO-----VKRAAQAAL-----DOYKLRQASIHNN---HVA 228
 Db 207 LVYIKIYIVLRRRRKRVNTRKSSRAFRANLKAFLKNGNTHPEMCKLCTVIMKNSGFPVN 266
 QY 229 RTDEAMPGRFQELD-SRLASGSPSEGISSEPVSAATTQTLEGSSSEVG----- 275
 Db 267 RRVFAARRAQELEMELSGSTPPERTRYSPIPSHHQLTLPDPSHHGLHSTPDSAPKE 326
 QY 276 -----DOINKKRAQMAEKSPPEASAKAQPIKGARRAPDSSEFGKTRMCFVFLCFAL 330
 Db 327 KNGHAKTVNPKIAKFIQSPNGKTRTS-LKTMRSRRLKSLQKKEKATQMLAIVLGVFI 385
 QY 331 SYIPFLNLTILDARVQAPRVVHMLAANLTWL---NGCINPVLYAAMNRQROAQSIL 385
 Db 386 CWLPFFTHILNIHCDG-NIPPVLYSAFTWLVYNSAVNPIIYTFNIEFRKAPLKIL 442

RESULT 8

A45121

alpha-1B adrenergic receptor - human

C:Species: Homo sapiens (man)

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Apr-2000
C/Accession: A45121; JC2332
R/Ramirez, C.S.; Denker, J.M.; Perez, D.M.; Gaivin, R.J.; Riek, R.P.; Graham, R.M.
J. Biol. Chem. 267, 21936-21945, 1992
A/Title: Genomic organization and expression of the human alpha 1B-adrenergic receptor.
A/Reference number: A45121; MUID:93016158; PMID:1328250
C/Accession: A45121
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-517 <RAM>
A/Cross-references: GB:M99590; NID:gl78211
A/Note: sequence extracted from NCBI backbone (NCBIP:116785)
A/Note: this translation is not annotated in GenBank entry HUMADREN, release 113.0 #dad
R/Reinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A/Title: Cloning, expression and characterization of human alpha adrenergic receptors al
A/Reference number: JC2331, MUID:94296402; PMID:8024574
C/Accession: JC2332
A/Molecule type: mRNA
A/Residues: 1-158, 'P', 160-244, 'H', 246-314, 'P', 316-380, 382-517 <WEI>
C/Genetics:
A/Gene: GDB:ADRA1B
A/Cross-references: GDB:127901; OMIM:104220
A/Map position: 5q31.1-5q33.2
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein
F/39-72/Domain: transmembrane #status predicted <TM1>
F/81-111/Domain: transmembrane #status predicted <TM2>
F/121-146/Domain: transmembrane #status predicted <TM3>
F/157-184/Domain: transmembrane #status predicted <TM4>
F/203-227/Domain: transmembrane #status predicted <TM5>
F/290-320/Domain: transmembrane #status predicted <TM6>
F/326-360/Domain: transmembrane #status predicted <TM7>
Query Match 14.0%; Score 286.5; DB 2; Length 517;
Best Local Similarity 24.9%; Pred. No. 7e-16;
Matches 96; Conservative 71; Mismatches 151; Indels 67; Gaps 12;
QY 23 AVSWGVA---VTCVGVNLTLLALAIQPKLRTNRLNLIANTLADLLCYTLLOPFSVD 79
DB 45 AISVGLVGAFLFAIVGNILVLSVACNRHURTPNYFIVNLAMADLLSLFTVPFSA 104
QY 80 TYLHLHWRGTCRCRVFGLLLFASNSVILTCLIALGRYLLIAHPKLPQVFSAGIVL 139
DB 105 LEVLGYVWLGRIEFDIAWADVLCCTASILSLCAISIDRYIGVYSLOQPTLVTRKAIL 164
QY 140 ALVSTVWVG-VAGFAPL--WPIVILVPVCTCFDRIRGRPYTILMGI-YFVLGLSSVG 195
DB 165 ALLSVVVLSTVIGIPLLGWK----BPAFNDXECGVTEEPFALFSLGSPYIPLAVIL 220
QY 196 IFCLHQRVQKRAAALDOYKLRQASIHNSHVARTDEAMPGRFOELDSLASGSPSEGIS 255
DB 221 VMCRVIVAKRTKLEAGVMKMS-----NSKELTIRHSKNFHE--- 262
QY 256 SEFVSAATTQLEGDSEVGDQINSKRAKQAEKSPPEASAKAQPIKGARRAPDSSEFG 315
DB 263 -----DTLSSTKAK-----GHNPRSSIAVKLFKFSRE-KKAATLIG 297
QY 316 KYTRMCFAPVLCFALSIPELL---INILDAVQARVVVHMLAANTLWNGCINPVLYAA 372
DB 298 IVVGM-----FVLWLPFFIALPGLSFLTKLPDANPKVFWLGYFNCLNPIIYFC 350
QY 373 MNRQFQAVGSIK--RGRSPFR 394
DB 351 SSKEFEKAVRILGCQCRGRRRRR 375
RESULT 9
T25837
hypothetical protein M03F4.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C/Accession: T25837

R/Fulton, L.
submitted to the EMBL Data Library, July 1996
A/Description: The sequence of C. elegans cosmid M03F4.
A/Reference number: Z20097
A/Accession: T25837
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-592 <FUL>
A/Cross-references: EMBL:U64601; PIDN:AAB04573.1; GSPDB:GN00028; CESP:M03F4.3
A/Experimental source: strain Bristol N2; clone M03F4
C/Genetics:
A/Gene: CESP:M03F4.3
A/Map position: X
A/Introns: 29/3; 106/3; 169/1; 212/2; 327/2; 358/2; 393/3; 464/3; 503/1; 546/3
C/Superfamily: octopamine receptor type 1
Query Match 14.0%; Score 286.5; DB 2; Length 592;
Best Local Similarity 22.5%; Pred. No. 8.2e-16;
Matches 111; Conservative 73; Mismatches 184; Indels 125; Gaps 18;
QY 17 LGYRYAVSWGVAVVGTV-GNVLTLLALAIQPKLRTNRLNLIANTLADLLCYTLLOP 75
DB 95 LGIHDVFIALFLVMLILLTIFGNILVLSVVVYKRMFTTNILTSLATADLLVGLVMP 154
QY 76 FSDVTYLHLH-WRTGATFCRVFGLLLFASNSVILTCLIALGRYLLIAHPKLPQVFS 134
DB 155 MSLLDLLNHRWPLGRFLCRWATSDVLLCTASILNLCVLSLDYFALTSPKYPRTSR 214
QY 135 KGIVALVSTVWVGVAFLPWIILVP-----VVCTCSFDRIRGRP 177
DB 215 KMAAGLLTAVWAIISFVVCSPW---VIPSNLFDNNNTGSSSEDFKCAYS-ESVAYRI 269
QY 178 YTT-----ILMGIYF-----VLGLSSVGIFYCLIHQVQKRAAALDOYKLR 218
DB 270 YSALGSFYLPLLVMLFVYFKFRVASEREALMRSVGT--CRLSNRLTKTQCKNQNNLR 327
QY 219 QAS-----IHSNH-----VARTDEAMPGRFOELDSLASGSPSEGISSE 257
DB 328 TASAPHSRTRVQVNHNGRVNYSVRPVEYANRVENSLKPSHERFDSTDCEDSPNGDSLE 387
QY 258 PVSAAAT-----QTLGDSSEVGDQIN----- 279
DB 388 ---AGTTCNISMLVTPPPNGLOKEAKNSMERSCHSLADIVNSADIPVRKNTEGVGAPS 444
QY 280 -SKRAKQK-AEKSPPEASAKAQ---PIKGARRAPDSSE-----FGKVTMCFAPVLCF 328
DB 445 LSKRARCQNRALQPNLLQKAHEHVQINGPCGKAVGSKKVMYMRERKALKTIGIVLGF 504
QY 329 ALSYTPFLLNILDARVQAP---RVVHMLAANTLW---NGCINPVLYAAMNQPRQAY 381
DB 505 IICWMPFFIMYLVEFISDPVAESPVIYITSEFFLWLGYSVNLNPIIYTMNGDFRCF 564
QY 382 GSILKGRSPFR 394
DB 565 RDLISFGCVQHHR 577
RESULT 10
DYM5D2
dopamine receptor D2 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C/Accession: S13921; JH0452; JH0453
R/Montmayeur, J.P.; Bausero, P.; Amlaiky, N.; Maroteaux, L.; Hen, R.; Borrelli, E.
FEBS Lett. 278, 239-243, 1991
A/Title: Differential expression of the mouse D(2) dopamine receptor isoforms.
A/Reference number: S13921; MUID:91122293; PMID:1991517
A/Accession: S13921
A/Molecule type: mRNA
A/Residues: 1-444 <MON>
A/Cross-references: EMBL:X55674; NID:950648; PIDN:CAA39209.1; PID:950649
R/Mack, K.J.; Todd, R.D.; O'Malley, K.L.
J. Neurochem. 57, 795-801, 1991

A;Title: The mouse dopamine D2A receptor gene: sequence homology with the rat and human
A;Reference number: JH0452; MUID:91318281; PMID:1861151
A;Accession: JH0452
A;Molecule type: DNA
A;Residues: 1-24, 'C', 26-28, 'P', 30-88, 'R', 90-103, 'S', 105-270, 'P', 252-444 <MAC>
A;Note: the authors translated the codon CAG for residue 16 as Glu
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;1-444/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-241/271-444/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;38-59/Domain: transmembrane #status predicted <TM1>
F;71-94/Domain: transmembrane #status predicted <TM2>
F;109-130/Domain: transmembrane #status predicted <TM3>
F;152-174/Domain: transmembrane #status predicted <TM4>
F;188-210/Domain: transmembrane #status predicted <TM5>
F;211-374/Domain: intracellular #status predicted <CYT>
F;375-398/Domain: transmembrane #status predicted <TM6>
F;407-430/Domain: transmembrane #status predicted <TM7>
F;5-17-23/Binding site: carboxydrate (Asn) (covalent) #status predicted
F;107-182/Disulfide bonds: #status predicted
F;147,148,228,229,355,360,365/Binding site: phosphate (Ser) (covalent) #status predicted
F;225,373/Binding site: phosphate (Thr) (covalent) #status predicted
F;444/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 13.9%; Score 283.5; DB 1; Length 444;
Best Local Similarity 25.6%; Pred. No. 1e-15;
Matches 112; Conservative 70; Mismatches 185; Indels 71; Gaps 16;

QY 2 WNSDANFSCVHESVLGYRYVAVGVVAVTGVGNVLLTALAIQPKLRTFNLLIAN 61
DB 22 FNGSEGRADRH-----YNYVAMLLTLLIFII-VFGNVLCMAVSREKALQTTNVLVS 75

QY 62 LTLADLYCTLLQPFSDVTLHL--HWRTGATPCRVGGLLFASNSVILTLCLIALGRY 119
DB 76 LAVADLLVATLVMPVW--YLEVVGEWKFRIHCDIFVTLVDMCTASILNLCASIDRY 133

QY 120 LLIAHPKLPFOVFAKGIIVLALVS-TWVGVASPAFLPIVPIVVPVCTGSPDRIRGRPY 178
DB 134 TAVAMPMLYNTRYSSKRRVTVMIAIWMVLSFTISCPL-----LFLGNLTQNECIANPA 188

QY 179 TTLIMGI-----YFVLGLSVGFYCLIHQ-----VKRAAQL-----D 213
DB 189 FWTYSIVSFYVPIVILLVIKIIYVLRKRVKRVNTRKSRFRANLKTPLKGNCTHPE 248

QY 214 QYKLQASIHNS-----HVARTDAMPGRFQELD-SRLASGSPSEGISSEPVSAATQTLL 267
DB 249 DMKLCITVMKSNGSFPVNRREMDAR--RAQELMEMLSSTSPERTRYSPIPPSSHQLT 306

QY 268 EGDSESVG-----DOINSKRAQMAEKSPPEASAKAQDIKGRAPDS 310
DB 307 LPDPSHGLHNSPDSPAKPKNGHAKIVNPRIAKFETQMPNGKTRTS-LKTMSSRKLS 365

QY 311 SSBEGKTRMCFAYFLCFALSYIPFLNLTLDARVQAPRVVHMLAANLTWL---NGCINP 367
DB 366 QREKKATQMLAIVLGVFICWIPFPFTTHLNIHDCD-NIPPVLYSAFTWLVGNSAVNP 424

QY 368 VLYAAMNRQFQAYGSL 385
DB 425 IIVTTFNIEFRKAPMKIL 442

RESULT 11
S08146
dopamine receptor D2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text change 22-Jun-1999
C;Accession: S08146; S19610; S07791; S09040; S09097; S19251; S08145; A34046; A34046; A34046; A34046
R;Monsa Jr., F.J.; McVittie, L.D.; Gerfen, C.R.; Mahan, L.C.; Sibley, D.R.
Nature 342, 926-929, 1989
A;Title: Multiple D2 dopamine receptors produced by alternative RNA splicing.
A;Reference number: S08146; MUID:90081873; PMID:2480527
A;Accession: S08146
A;Molecule type: mRNA

A;Residues: 1-444 <MON>
A;Cross-references: EMBL:X17458
R;Chio, C.L.; Hess, G.F.; Graham, R.S.; Huff, R.M.
Nature 343, 266-269, 1990
A;Title: A second molecular form of D2 dopamine receptor in rat and bovine caudate nucleus.
A;Reference number: S08163; MUID:90136899; PMID:2137198
A;Accession: S19610
A;Molecule type: mRNA
A;Residues: 1-444 <CHI>
R;Runow, J.R.; van Tol, H.H.M.; Grandy, D.K.; Albert, P.; Salon, J.; Christie, M.; MacKenzie, R.G.
Nature 336, 783-787, 1988
A;Title: Cloning and expression of a rat D(2) dopamine receptor cDNA.
A;Reference number: S07791; MUID:89082643; PMID:2974511
A;Accession: S07791
A;Molecule type: mRNA
A;Residues: 1-241, 271-444 <BUN>
A;Cross-references: EMBL:X14028
R;Rao, D.D.; McKelvy, J.; Kebabian, J.; MacKenzie, R.G.
FEBS Lett. 263, 18-22, 1990
A;Title: Two forms of the rat D(2) dopamine receptor as revealed by the polymerase chain reaction.
A;Reference number: S09040; MUID:90235966; PMID:2139615
A;Accession: S09040
A;Molecule type: mRNA
A;Residues: 1-98, 'D', 100-172, 'R', 174-179, 'G', 181-444 <RAO>
A;Cross-references: GB:X53278; NID:9288117; PIDN:CAA37373.1; PID:9288118
R;O'Dowd, B.F.; Nguyen, T.; Tirpak, A.; Jarvie, K.R.; Israel, Y.; Seeman, P.; Niznik, H.F.
FEBS Lett. 262, 8-12, 1990
A;Title: Cloning of two additional catecholamine receptors from rat brain.
A;Reference number: S09096; MUID:90201380; PMID:2138567
A;Accession: S09097
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 126-303 <ODO>
R;Idal Toso, R.; Sommer, B.; Ewert, M.; Herb, A.; Pritchett, D.B.; Bach, A.; Shivers, B.D.
EMBO J. 8, 4025-4034, 1989
A;Title: The dopamine D2 receptor: two molecular forms generated by alternative splicing.
A;Reference number: S09618; MUID:90076122; PMID:2531656
A;Accession: S19251
A;Molecule type: mRNA
A;Residues: 175-299 <DAL>
R;Giros, B.; Sokoloff, P.; Martres, M.P.; Riou, J.F.; Emorine, L.J.; Schwartz, J.C.
Nature 342, 923-926, 1989
A;Title: Alternative splicing directs the expression of two D2 dopamine receptor isoforms.
A;Reference number: S08145; MUID:90081872; PMID:2531847
A;Accession: S08145
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 239-272 <GIR>
R;Miller, J.C.; Wang, Y.; Filer, D.
Biochem. Biophys. Res. Commun. 166, 109-112, 1990
A;Title: Identification by sequence analysis of a second rat brain cDNA encoding the dopamine D2 receptor.
A;Reference number: A34046; MUID:90147685; PMID:2137336
A;Accession: A34046
A;Molecule type: mRNA
A;Residues: 242-270 <MIL>
A;Cross-references: GB:M32241; NID:9203902; PIDN:AAA41074.1; PID:9203904
R;Taylor, P.L.; Inglis, J.D.; Sidne, K.A.
submitted to the EMBL Data Library, October 1990
A;Description: 5' untranslated region of rat pituitary dopamine D2(B) receptor contains a stop codon.
A;Reference number: S21548
A;Accession: S21548
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-444 <RAY>
A;Cross-references: EMBL:X56065; NID:956063; PIDN:CAA39543.1; PID:956064
C;Genetics:
A;Introns: 241/3; 270/3; 381/1
A;Note: the list of introns may be incomplete
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;1-444/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-241, 271-444/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;38-59/Domain: transmembrane #status predicted <TM1>

F:71-94/Domain: transmembrane #status predicted <TM2>
F:109-130/Domain: transmembrane #status predicted <TM3>
F:152-174/Domain: transmembrane #status predicted <TM4>
F:188-210/Domain: transmembrane #status predicted <TM5>
F:211-374/Domain: intracellular #status predicted <INT>
F:375-398/Domain: transmembrane #status predicted <TM6>
F:407-430/Domain: transmembrane #status predicted <TM7>
F:5,17,23/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:107-182/Disulfide bonds: #status predicted
F:228,229/Binding site: phosphate (Ser) (covalent) #status predicted
F:444/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 13.9%; Score 283.5; DB 1; Length 444;
Best Local Similarity 25.6%; Pred. No. 18-15;
Matches 112; Conservative 70; Mismatches 185; Indels 71; Gaps 16;

QY 2 WNSDDANFSCYHESVLGYRYVAVSVGVAVVAVGTGVNLTLLALAIQPKLIRFNLLIAN 61
DB 22 FNGSEKADPH-----YNYVAMLLTLFII-VGVNLVAVSREKALQTTNYLVLS 75

QY 62 LTLADLLYCTLLQPPSVDTYHLH--HWRTGATFCRVFGLLLFASNSVSLTLCIALGRY 119
DB 76 LAVADLLVATLMPWV--YLEVVGWKFESRIHCDIFVTLDMVMCTASINLCAISIDRY 133

QY 120 LLIAPKLPQVFSAGIVLALVS-TWVGVASFAPLWFIYILVPVCTCFDRIGRPY 178
DB 134 TAVAMNLTNRYSSKRRVTWIAIVVLSFTISCPD-----LFGNNTDQNECIANPA 188

QY 179 TTILMGI-----YFVLGSSVGIFCYLHQRQ-----VKRAAQAAL-----D 213
DB 189 FVYSSIVSVFVPIVTLVYIKIYIVLKRKRKRVNTRKSSRAFRANLXTPILKGNCTHPE 248

QY 214 QYKLRASIHSN-----HVARTDEMPGRFOELD-SRLASGGPSEGISSEPVSAATQTL 267
DB 249 DMKLCTVIMKNSGFFVNNRRMDAAR--RAQELMEMLSSTPPETRYSPIPPSSHQUT 306

QY 268 EGDSEVSG-----DQINSKAKQWAEKSPPEASAKAQPFIKGRARRAPDS 310
DB 307 LPDPSSHGLHNSPDSAPKEKNGKHAIVNPRIAKPFEIQTMPNGKTRTS-LXTMSRKL 365

QY 311 SSEFGKVTMCFVFLCPALSYTPFLLNLLIDARVQAPRVHMLAANLTWL---NGCINP 367
DB 366 QQKEKATQMLAIVLGVFFIICWLPFFITHILNHDC-NIPPVLSAFTWLVGVNSAVNP 424

QY 368 VLYAAMNROFROAYGSIL 385
DB 425 IIVTTNIEFRKAFMKIL 442

RESULT 12
A35375
alpha-1-adrenergic receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C:Accession: A35375
R:Schwinn, D.A.; Lomasney, J.W.; Lorenz, W.; Saklat, P.J.; Fremeau Jr., R.T.; Yang-Feng, J. Biol. Chem. 265, 8183-8189, 1990
A:Title: Molecular cloning and expression of the cDNA for a novel alpha-1-adrenergic receptor
A:Reference number: A35375; MUID:90243698; PMID:1970822
A:Accession: A35375
A:Molecule type: mRNA
A:Residues: 1-466 <SCH>
A:Cross-references: GB:J05426; NID:g162663; PIDN:AAA30374.1; PID:g162664
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

Query Match 13.8%; Score 281.5; DB 2; Length 466;
Best Local Similarity 23.0%; Pred. No. 1.6e-15;
Matches 95; Conservative 82; Mismatches 153; Indels 83; Gaps 13;

QY 3 NSSDANFSCYHESVLGYRYVAVSVGVAVVAVGTGVNLTLLALAIQPKLIRFNLLI 59
DB 7 NASDSS-NCTHPPPVNIKAILGLVILGLLGLVILGLVILSVACHSLHLSVTHYVI 65

QY 60 ANUTLADLLYCTLLQPPSVDTYHLHWRGTATFCRVFGLLLFASNSVSLTLCIALGRY 119
DB 66 VNLAVADLLTSTVLPFSALFEILGYWAFGRVFCNVAAVAVDVLCTASINGLCIISIDRY 125

QY 120 LLIAPKLPQVFSAGIVLALVS-TWVGVASFAPLWFIYILVPVCTCFDRIGRPY 175
DB 126 IGVSYPRIYTYVTKRGLMALICVWALSIVISGPIFGWRQPAPEDETIC-----QINE 180

QY 176 RPYTTILMGI-YFVLGSSVGIFCYLHQRQVKAQAALDOYKLRQASIHSHNVARTDEAM 234
DB 181 EPGVFLFSALGSFYVPLTIILVMYCRYVYVAVKRESGL----- 218

QY 235 PGRFQELDSLASGSPSEGISSEPVSAATQTQLESDSEVGDQINSKEAKQMAEKSPPEA 294
DB 219 -----KSGKTD-----KSDSEQVTLRIHRQNA-QVGGSGVTSA 251

QY 295 SAK-----AQPIKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNLLNIDA--RVQA 347
DB 252 KNTKTHFSVRLKFSREK-----KAAKTGLGVVGCFLVCLWLPFFLVMPISGFPDPRP 303

QY 348 PRVHMLAANLTWNLGNCINPVLYAAMNROFROAYGSI-----LKRGRPSFRL 395
DB 304 SETVFKIAFWLGLYNSCINPIIYPCSSQEFKAFQNVIRIQCLRRKQSSKHTL 356

RESULT 13
S58868
G protein-coupled receptor GCRI - migratory locust
C:Species: Locusta migratoria (migratory locust)
C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Nov-2000
C:Accession: S58868; S58869
R:Vanden Broeck, J.; Vulsteke, V.; Huybrechts, R.; De Loof, A. J. Neurochem. 64, 2387-2395, 1995
A:Title: Characterization of a cloned locust tyramine receptor cDNA by functional expression
A:Reference number: S58868; MUID:95279966; PMID:7760020
A:Accession: S58868
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-484 <VAN>
A:Cross-references: EMBL:X69520; NID:g871404; PIDN:CAA49268.1; PID:g871405
A:Accession: S58869
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-307, 'D', 309-338, 'K', 340-484 <VA2>
A:Cross-references: EMBL:X69521; NID:g871406; PIDN:CAA49269.1; PID:g871407
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
C:Superfamily: octopamine receptor type I
C:Keywords: G protein-coupled receptor

Query Match 13.7%; Score 280; DB 2; Length 484;
Best Local Similarity 24.5%; Pred. No. 2.2e-15;
Matches 111; Conservative 63; Mismatches 187; Indels 92; Gaps 17;

QY 15 SVLGYRYVAVSVGVAVVAVGT-----TVGNVLTLLALAIQPKLIRFNLLIANLTAD 66
DB 38 SVLGVRLAVPWEVAVTAVSVLSLILITVGNVILVLSVFTYKPLRVQNFVIVSLAVAD 97

QY 67 LLYCTLLQPPSVDTYHLHWRGTATFCRVFGLLLFASNSVSLTLCIALGRYLLIAHPK 126
DB 98 LTVAVLVNPFNVAVSLIQRWVFGIVCKWMLTCDVLCCTASILNLCALDRYWAITDPI 157

QY 127 LPQVFSAGIVLALVS-TWV-VYASAPLI-----WPIYI--LVPVCTCFDRIGRPY 178
DB 158 NYAQKRTLRRLAMTAGVLLSGVSISSPPLIGWMDWPFMFNDTP-----COLTEBQGVYI 213

QY 179 TTILMGIY---FVLGSSVGIFCYLHQRVKAQA-----QALDQYKLRQA----- 220
DB 214 YSLGSGFFIPIFIMTVIVVEIFIATKRLRLERAKSKLNSAMKQQAQVAVSSVPESHQ 273

QY 221 ---STHSHN-----VARTDEAMPGRF-----QELDSRLAS 247
DB 274 ESVSSETNHNELPPPPAPPSPKSKRKTKKKQKQAAEEGRFLAPAVAEEDSVTDNSVS 333

[illegible]

Db 297 FPPDFKPSFTVKIVFWLGYLNSCINPIIYPCSSQEFKKAFONVLRIOCLRRROSSKHAL 356

Search completed: September 24, 2004, 08:40:17
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 04:51:55 ; Search time 24 Seconds
(without alignments)
859.158 Million cell updates/sec

Title: US-10-029-436-2

Perfect score: 2041

Sequence: 1 MNSSDANFSCYHESVLGYR.....FRQAYGSLKRGPSFRLH 396

Scoring tables: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	338	16.6	392	1	TRE1 DROME
2	298	14.6	436	1	D2DR_MELGA
3	291	14.3	442	1	D2DI_XENLA
4	290	14.2	443	1	D2DR_HUMAN
5	290	14.2	443	1	D2DR_PANTR
6	288.5	14.1	466	1	A1AA_MOUSE
7	288.5	14.1	515	1	A1AB_MESAU
8	288	14.1	444	1	D2DR_BOVIN
9	287.5	14.1	515	1	A1AB_RAT
10	287	14.1	443	1	D2DR_CERAE
11	286.5	14.0	519	1	A1AB_HUMAN
12	283.5	13.9	444	1	D2DR_MOUSE
13	281.5	13.8	466	1	A1AA_BOVIN
14	281	13.8	484	1	OAR2_LOCOMI
15	280	13.7	484	1	OAR1_LOCOMI
16	279.5	13.7	514	1	A1AB_MOUSE
17	278.5	13.6	466	1	A1AA_RAT
18	278.5	13.6	466	1	A1AA_CAVPO
19	274	13.4	466	1	A1AA_HUMAN
20	273.5	13.4	400	1	D3DR_HUMAN
21	272.5	13.4	463	1	D2DR_FUGRU
22	272.5	13.4	463	1	D2DR_ORVLA
23	272	13.3	470	1	A1AA_MOUSE
24	271.5	13.3	562	1	A1AD_RAT
25	270.5	13.3	561	1	A1AD_RAT
26	268.5	13.2	400	1	D3DR_CERAE
27	267.5	13.1	446	1	D3DR_MOUSE
28	267.5	13.1	446	1	D3DR_RAT
29	267.5	13.1	583	1	ML1X_MOUSE
30	266	13.0	400	1	B3AR_MOUSE
31	266	13.0	425	1	OX1R_HUMAN
32	264.5	13.0	508	1	GL01_HUMAN
33	259	12.7	363	1	5H1E_PANTR

RESULT 1

TRE1 DROME	34	259	12.7	365	1	5H1E HUMAN	P28566 homo sapien
ID TRE1 DROME	35	259	12.7	452	1	GASR_RAT	P30553 rattus norv
AC Q9NDM2; Q95NV3; Q95NV9; Q9NKZ6; Q9W498;	36	257.5	12.6	576	1	ALAD_RABIT	O02666 oryctolagus
DT 28-FEB-2003 (Rel. 41, Created)	37	257	12.6	400	1	B3AR_RAT	P26255 rattus norv
DT 28-FEB-2003 (Rel. 41, Last sequence update)	38	255.5	12.5	416	1	OX1R_RAT	P56718 rattus norv
DT 10-OCT-2003 (Rel. 42, Last annotation update)	39	255	12.5	346	1	ML1C_CHICK	P49288 gallus gall
DE Gustatory receptor Trehalose 1 (Trehalose receptor 1).	40	255	12.5	458	1	5H2C_HUMAN	P28335 homo sapien
GN TRE1 OR CG3171.	41	254.5	12.5	458	1	A2AC_MOUSE	Q01337 mus musculu
OS Drosophila melanogaster (Fruit fly).	42	254.5	12.5	458	1	A2AC_RAT	P22086 rattus norv
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	43	254	12.4	405	1	B3AR_SHEEP	Q9XT58 ovis aries
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	44	254	12.4	613	1	ML1X_HUMAN	O13585 homo sapien
OC Ephydroidea; Drosophilidae; Drosophila.	45	253	12.4	427	1	CKRP_RABIT	O97772 oryctolagus
OX NCBI_TaxID=7227;							
RN [1]							
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.							
RC TISSUE=labial palps;							
RX MEDLINE=20342437; PubMed=10884225;							
RA Ishimoto H., Matsumoto A., Tanimura T.;							
RT "Molecular identification of a taste receptor gene for trehalose in							
RT Drosophila.";							
RL Science 289:116-119(2000).							
RN [2]							
RP SEQUENCE FROM N.A., FUNCTION, AND VARIANTS.							
RC STRAIN=HG84, Shanghai, Singapore, Tananarive, w cv, and w cx;							
RX MEDLINE=21450540; PubMed=11566105;							
RA Ueno K., Ohta M., Morita H., Mikuni Y., Nakajima S., Yamamoto K.,							
RA Isono K.;							
RT "Trehalose sensitivity in Drosophila correlates with mutations in and							
RT expression of the gustatory receptor gene Gr5a.";							
RL Curr. Biol. 11:1451-1455(2001).							
RN [3]							
RP SEQUENCE FROM N.A.							
RC STRAIN=Berkley;							
RC MEDLINE=20196006; PubMed=10731132;							
RA Adams M.D., Ceiniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,							
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,							
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,							
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,							
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,							
RA Wan X.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,							
RA April J.F., Agayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,							
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,							
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,							
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,							
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,							
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,							
RA de Pabloe B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,							
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,							
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,							
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,							
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,							
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,							
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,							
RA Talali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,							
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,							

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirski R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000).
 RN [4]
 RP REVISIONS.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.K., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley; TISSUE=Embryo;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celisner S.E.;
 RT "A *Drosophila* full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -!- FUNCTION: Taste receptor sensitive to trehalose.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -!- TISSUE SPECIFICITY: Expressed ubiquitously in adult tissues.
 CC Highest expression levels are seen in taste sensory cells of the
 CC labellar chemosensory neurons and tarsi.
 CC -!- DEVELOPMENTAL STAGE: Expressed throughout embryo to adult
 CC stages.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the ENBL oustation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC
 CC ENBL; AB034204; BA95353.1;
 CC ENBL; AB042625; BA96500.1;
 CC ENBL; AB066613; BA868237.1;
 CC ENBL; AB066614; BA868238.1;
 CC ENBL; AB066615; BA868239.1;
 CC ENBL; AB066616; BA868240.1;
 CC ENBL; AB066617; BA868241.1;
 CC ENBL; AB066618; BA868242.1;
 CC ENBL; AB030335; AA246059.2;
 CC ENBL; AY070980; AA44602.1;
 CC FlyBase; FBgn0046687; Trel.
 CC GO; GO:0016021; C:integral to membrane; NAS.
 CC GO; GO:0008527; F:taste receptor activity; IMP.
 CC GO; GO:0001582; P:sweet taste perception; IMP.
 CC InterPro; IPR002026; GPCR_Rhodopsin.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSIN.

DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Polymorphism; Multigene family.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 60 1 (POTENTIAL).
 FT DOMAIN 61 73 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 94 2 (POTENTIAL).
 FT DOMAIN 95 110 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 111 131 3 (POTENTIAL).
 FT DOMAIN 132 156 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 157 177 4 (POTENTIAL).
 FT DOMAIN 178 202 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 203 223 5 (POTENTIAL).
 FT DOMAIN 224 268 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 269 289 6 (POTENTIAL).
 FT DOMAIN 290 302 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 303 323 7 (POTENTIAL).
 FT DOMAIN 324 392 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARIANT 7 7 M -> MDXMGGM (IN STRAINS HG84, SINGAPORE
 FT AND W CV).
 FT VARIANT 12 12 F -> I (IN STRAINS HG84, SINGAPORE
 FT AND W CV).
 FT VARIANT 348 348 L -> M (IN STRAINS SHANGHAI AND
 FT TANANARIVE).
 FT CONFLICT 226 226 L -> P (IN REF. 1).
 FT SEQUENCE 392 AA; 43843 MW; 41A58C69479BFD4 CRC64;
 Query Match 16.6%; Score 338; DB 1; Length 392;
 Best Local Similarity 25.9%; Pred. No. 3.3e-16;
 Matches 106; Conservative 67; Mismatches 140; Indels 96; Gaps 14;
 QY 7 ANFCV-HESVLGYRYAVSVGVVAVVGVTVGNVLTALALQPKLR---TRNLLAN 61
 DB 25 ATQSYPHSATU---FAAISACVFVTI-GVGNLTLLALKSPTRHATAP---VIS 77
 QY 62 IFLADLYCTLLQPPSVDTYLLHWRGTGATFCRVGLLFFASNSVSLTCLIALGRYLL 121
 DB 78 LSIIDLLFCPSPLTAVRFFQESWTFGTTLCKIPFVYGNVAVSLMGVITLRYIL 137
 QY 122 IAHPLKLPQVPSAKGIVLALVSTVGVVASAP---LWPIYILVPVVTCSFDRISGRP 177
 DB 138 IACHSRYSCIVKPKPITLQLLFWAVSELLLPLLPGIWMGMDGDEATFSTILKSGRS 197
 QY 178 YTTILMGYFVGLSSVGIFCLIHQVRAAQALDQYKLFQASIHSHNHVARTDEAMPGR 237
 DB 198 IKKTLFVIGLPCIVIVSYCVITV-----LHQKKIRNH-----DN 237
 QY 238 FOELDSRLASGPGSEGISSEPVSAATOTLEGDSSEVDQINSKRAQMAKSPPEASAK 297
 DB 238 FO-----IAAA-----KGSSSGGSGSYMTTCTTKAR-----264
 QY 298 AQPICKGARRADSSSEFGKVRMCFAPVFLCPALSVIPFLNLIL-DARVOAPRVVHMLAA 356
 DB 265 -----EDNRLIVMMVTIFLCFLVCLPLMLANVVDDERNISYPWHLIAS 309
 QY 357 NLTWINGCINPVLYAAMNRQFQAY-----GSLKRGPR-RSFHR 394
 DB 310 VNAWASSVINPIIYAASNNRYRVAYKIFALLKFWGPEPLSPMPSPRYHQ 358
 RESULT 2
 D2DR MELGA STANDARD; PRT; 436 AA.
 ID D2DR MELGA AC 073810;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE D(2) dopamine receptor.
 GN DRD2.
 OS *Meleagris gallopavo* (Common turkey).
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;

[illegible]

```

227 GLDSDTHAPLKDKCTHPENVKLTGVIVKSNQSGFQVKNRKRCEAEHSIKMEEMKMSSTSPPE 286
242 DSRLASGGSPSEGISSEPPVAAITQTLE-----GDSSEVGQINSKRAKQMAEKSPPE 293
287 RTIVKAAAFSNHCLVVPV-ASRSILDSGKVEKNHAK-----NLHTAKVFEIQSMBN 340
294 ASAKAQPIKGRAPPDSSEFGKVTMCFALVCLFALSIVIPELLNILDARVQARVVHM 353
341 GKTRSTLLKAMNRRKLSQOKEKATQMLAIVLGVFTIICWLPPFTIHLNMHCDCNIPPAM 400
354 LAANLFWL--NGCINPVLVYAMNRQFROAGYSIL 385
401 YSA-FTWLGVNVSAVNPITTYTFNIEFRKAFMKIL 434

RESULT 3
D2D1_XENLA
ID _D2D1_XENLA STANDARD; PRT; 442 AA.
AC P24628;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE D(2) dopamine receptor 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
RN NCBI_TaxID=8355;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91200321; PubMed=1826663;
RA Martens G.J.W., Moelhuizen H.O.F., Groeneveld D., Roubos E.W.;
RT "Cloning and sequence analysis of brain cDNA encoding a Xenopus D2
RT dopamine receptor.";
RL FEBS Lett. 281:85-89(1991).
CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors
CC for dopamine. The activity of this receptor is mediated by G
CC proteins which inhibits adenylyl cyclase. In xenopus D2r is
CC involved in the regulation of the melanotrope cells of the
CC intermediate pituitary during background adaptation of the animal.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Brain; pituitary.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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Query Match	14.6%;	Score 298;	DB 1;	Length 436;
Best Local Similarity	25.5%;	Pred. No. 2e-13;		
Matches 116;	Conservative .66;	Mismatches 173;	Indels 100;	Gaps 17;
QY	2	WNSSDANFS-CVHESVLG----	YRVAVSWGVVAVTGVGNVLVLTLLALAIQPKLRITFN	56
DB	9	YNTGRDNWSEPNYESAQQPKQNYAYAVLLTLLIFVI-VFGNVLVCMAVSREKALQTTTN		67
QY	57	LLIANLTADLYCTLLQPFSDVTYHL--HWRTGATCFRVFGLLLFASNSVSLTCLJ		114
DB	68	YLIVSLAVADLLVATLVMPWV--YLEVVGWEFRSRIHCDIEFTVLDMVCTASILLNLCAL		125
QY	115	ALGRVLLIAHPKLFQPVFSAGKIVIALVS-TVVVGVAFFAPLW-----PI		158
DB	126	SIDRYTAAAMPVLNYNTRYSSKRRVTVMIACVWLSPAISSPILFGINKADERCIANPA		185
QY	159	YIL-----VPVCTCSFDRIERGEPTTILMGIFYVLGLSSVGIFYCLIHQVKRAAQ		210
DB	186	FVYSSVSGFYVFFIVT-----LLVVQIVWJLRRR-----KHETKRSSH		226
QY	211	ALD-----QYKLRQASIHNN-----HVARTDEAMPGRFOEL		241

CC	or send an email to license@sb-sib.ch).
CC	-----
DR	EMBL; X59500; CAA42088.1; -
DR	PIR; S14827; DYXLD2.
DR	InterPro; IPR000276; GPCR_Rhodopsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PRG0237; GPCRHHODOPSN.
DR	PROSITE; PS00237; G-PROTEIN RECEP_F1_1; 1.
DR	PROSITE; PS00262; G-PROTEIN RECEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Multigene family.
FT	DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 32 54 1 (POTENTIAL).
FT	DOMAIN 55 65 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 66 91 2 (POTENTIAL).
FT	DOMAIN 92 102 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 103 124 3 (POTENTIAL).
FT	DOMAIN 125 145 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 146 168 4 (POTENTIAL).
FT	DOMAIN 169 180 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 181 204 5 (POTENTIAL).

RN SEQUENCE FROM N.A. (ISOFORM 3).
 RA Sawa M., Sato T., Okouchi I., Arita M., Putani K., Matsumoto S.,
 RA Teutumi S., Aburatani H., Asai K., Akiyama Y.,
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP Kadd K.K.;
 RA Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Lung;
 RC MEDLINE=2238257; PubMed=12477932;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zebberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN VARIANT CVS-311.
 RP MEDLINE=94071859; PubMed=7902708;
 RX Itokawa M., Arinami T., Futamura N., Hamaguchi H., Toru M.;
 RA "A structural polymorphism of human dopamine D2 receptor,
 RT D2(Ger311->Cys).";
 RL Biochem. Biophys. Res. Commun. 196:1369-1375(1993).
 RN VARIANT MD ILE-154.
 RP MEDLINE=99238502; PubMed=10220438;
 RX Klein C., Brin M.F., Kramer P., Sena-Esteves M., de Leon D.,
 RA Doherty D., Bressman S., Fahn S., Breakfield X.O., Ozelius L.J.;
 RT "Association of a missense change in the D2 dopamine receptor with
 RT myoclonus dystonia."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5173-5176(1999).
 CC -1- FUNCTION: This is one of the five types (D1 to D5) of receptors
 CC for dopamine. The activity of this receptor is mediated by G
 CC proteins which inhibit adenylyl cyclase.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=D2(Long);
 CC IsoId=P14416-L; Sequence=Displayed;
 CC Name=2; Synonyms=D2(Short);
 CC IsoId=P14416-2; Sequence=VSP_001870;
 CC Name=3; Synonyms=D2(Longer);
 CC IsoId=P14416-3; Sequence=VSP_008511;
 CC -1- DISEASE: It has been suggested that DRD2 is involved in
 CC psychiatric disorders; especially in schizophrenia. It has also
 CC been implicated in susceptibility to alcoholism.
 CC -1- DISEASE: Defects in DRD2 are associated with myoclonus dystonia
 CC (MD) [MIM:159900]; also known as myoclonic dystonia or alcohol-
 CC responsive dystonia. MD is a movement disorder characterized by
 CC involuntary lightning jerks and dystonic movements and postures
 CC alleviated by alcohol. Inheritance is autosomal dominant.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC -----
 DR EMBL; M30625; AAA88024.1; -
 DR EMBL; X51645; CAB56463.1; -
 DR EMBL; X51646; CAB37869.1; -
 DR EMBL; X51362; CAB35746.1; -
 DR EMBL; M29066; AAA52761.1; -
 DR EMBL; S62137; AAB26819.1; -
 DR EMBL; S69899; AAB20571.1; -
 DR EMBL; S58589; AAB26274.1; -
 DR EMBL; S58577; AAB26274.1; JOINED.
 DR EMBL; S58584; AAB26274.1; JOINED.
 DR EMBL; S58586; AAB26274.1; JOINED.
 DR EMBL; S58588; AAB26274.1; JOINED.
 DR EMBL; AF176812; AAF61479.1; -
 DR EMBL; AB065860; BAC06078.1; -
 DR EMBL; AF050737; AAC87779.1; -
 DR EMBL; BC021195; AAH21195.1; -
 DR F18; S06417; DYHUD2
 DR FDB; L115; 28-FEB-01.
 DR Genew; HGNC:3023; DRD2.
 DR MIM; 126450; -
 DR MIM; 159900; -
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005882; C:intermediate filament; TAS.
 DR GO; GO:0004952; P:dopamine receptor activity; TAS.
 DR GO; GO:0004888; P:transmembrane receptor activity; TAS.
 DR GO; GO:0007212; P:dopamine receptor signaling pathway; TAS.
 DR GO; GO:0007195; P:dopamine receptor; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 Query Match 14.2%; Score 290; DB 1; Length 443;
 Best Local Similarity 25.8%; Pred. No. 7.3e-13;
 Matches 114; Conservative 65; Mismatches 183; Indels 80; Gaps 15;
 QY 2 WNSDANFSCYHESVLGYRYVAVSVVAVTGVNVLTLALLAIOFKLTRENLIFAN 61
 DB 22 FNGSDGKADRPH-----YNYATLTLIIAVI-VFGNVLCMAVSREKALQTTNYLIIVS 75
 QY 62 LTLADLLYCTLLQPPSVDTYUHL--HWRTGATFCRVFGLLLFASNSVSLTCLIALGRY 119
 DB 76 LAVADLLVATLVMPWV--YLEVVGEMKFSRHCDFVTLDEWMMCTASILNLCAISIDRY 133
 QY 120 LLIAHPKLPQVFGAKGIVLALVSTWVGVASAPLWPIYILVPVVCFSFDRIRGRPYT 179
 DB 134 TAVAMPMLYNTYRSKRRVTWIS--IVWLVSFT-----ISCPLLFGLNADQNE 181
 QY 180 TILMGIYFVLGLSSVGIF-----YCLIHQO-----VKRAQAL----- 212
 DB 182 CIIANPAFVYVSVSVFVPIVILLVYIKIYIVLRERRKRVNTRKSSRAFHLRAPLK 241
 QY 213 -----DQYKLRQASIHSN---HVARTEAMPGRFOELD-SRLASGGPSEGISSEPVSA 262
 DB 242 GNCTHPEDMKLCCTVIMKNSGFPVNNRRVVEARRAQAELEMELSTSPETRTISPSPS 301
 QY 263 ITQTLEGSSSEVG-----DOINSKRAKQMAEKSPPEASAKAQPIKGARR 306
 DB 302 HHQLTLPDPSSHHLHSTPDSPAKPEKNGHAKDHPKIAKIFEIQTWPNKTRTS-LKTMRSR 360
 QY 307 APDSSESGKVTMRCFAVFLCFALSYIFLLNLIDARVQPRVVHMLAANLWJL---NG 363
 DB 361 RKLQSQEKKATQMLAIVLGVFIICWLEFFFTIHLNTHCDC-NIPPLVLYSAFTMLGVYNS 419
 QY 364 CINPVLYAAMNRQPRQAYGSIL 385
 DB 420 AVNPPIYTFNIEFKAFKLIL 441

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Query Match      14.2%; Score 290; DB 1; Length 443;
Best Local Similarity 25.8%; Pred. No. 7.3e-13;
Matches 114; Conservative 65; Mismatches 183; Indels 80; Gaps 15;

QY 2 WNSDANFSCYHESVLGYRYAVSVGVVAVTGTGVNLTLLALAIQPKLRTRENFLLIAN 61
DB 22 FNGSDGKADPH-----YNYATLLTLLIATV-VFQNVLCVAVSREKALQTTNYLIVS 75
QY 62 LTLADLLYCTLLQPPSVDTYHL--HWRTGATFCVFGLLLPASNSVSLTLCIALGRY 119
DB 76 LAVADLLVATLVMPVWV--YLEVWGEWKFSTRICDIFVTLDVMMCTASILNLCASIDRY 133
QY 120 LLIAHPKLPFPQVSAKGIVLALVSTWVGVASFAPLWPIYILVPVVCSTCDIRGREPT 179
DB 134 TAVAMPMLNTRYSSKRRVTWIS--IVWVLSFT-----ISCPLLEGLNADQNE 181
QY 180 TILMGIFYVLGLSSVGIF-----YCLHRO-----VKRAAQAAL----- 212
DB 182 CIANPAFVYVSSIVSFVVPFTVTLVYIKIYIVLRKRKRVNTRKSRAPRAHLRAFLK 241
QY 213 -----DOYKLQASIHGN---HVAETDEAMPGRFOELD-SRLASGGPSEGISSEPVSA 262
DB 242 GNCTHPEDMKLCVTIMKNGSPFVNRVRVEARRAQELEMELMSTSPETRTYSPIPPS 301
QY 263 TTQTLEGSSEVG-----DQINSKRAKQMAEKSPPEASAKAQPIKGARR 306
DB 302 HHQLTLPDPSSHGLHSTPDSPAKPEKNGHAKDHPKIAKIFETQMPNGKTRTS-LKTM 360
QY 307 APDSSESGKVTMCFVFLCFALSYIFPLLNLILDARQAPRVVHMLAANLTW-----NG 363
DB 361 RXLSQCKKKATQMLAIVLGVFIICWLEPFTHILNIHCDC-NIPPVLYSAFTWLGYNV 419
QY 364 CINPVLYAAMNROPRQAYGSIL 385
DB 420 AVNPIIYTFNIEFRKAPFLKIL 441

RESULT 6
ALAA MOUSE STANDARD; PRT; 466 AA.
ID ALAA MOUSE STANDARD; PRT; 466 AA.
AC P97718: 054913;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE adrenergic receptor).
GN ADRA1A OR ADRA1C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=CD-1; TISSUE=Brain, and Kidney;
RX MEDLINE=98292316; PubMed=9630362;
RA Xiao L., Scofield M.A., Jeffries W.B.;
RT "Molecular cloning, expression and characterization of cDNA encoding a
RL mouse alpha1A-adrenoceptor.";
RN [2] Br. J. Pharmacol. 124:213-221(1998).
RP SEQUENCE OF 197-280 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96064818; PubMed=7595531;
RA Alonso-Blanco M.A., Zamanillo D., Casanova E., Ovalle S., Calvo P.,
RA Chinchetru M.A.;
RT "Molecular cloning of alpha 1d-adrenergic receptor and tissue
RT distribution of three alpha 1d-adrenergic receptor subtypes in
RT mouse.";
RL J. Neurochem. 65:2387-2392(1995).
CC -!- FUNCTION: This alpha-adrenergic receptor mediates its action by
CC association with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system. Its effect is mediated by G(q)
CC and G(11) proteins.

```


Db	263	KFSREK-----KAAXTLGIWGCFLVLCMLPFFLVMPIGS	296
Qy	344	---RVQAPRVVHMLANLTLNWCINPVLYAAMNRQFRQAYGSI-----LKRGERSFHRL	395
Db	297	FFPNFKPETVFYKIVFWLGLNSCINPIIYPCSSQBKKAFQNVLRIQCLERRQSSKHAL	356
 RESULT 7 AIAB_MESAU STANDARD; PRT; 515 AA.			
ID	AIAB_MESAU	STANDARD;	PRT; 515 AA.
AC	P18841;		
DT	01-NOV-1990 (Rel. 16, Created)		
DT	01-NOV-1990 (Rel. 16, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
GN	Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).		
DN	ADRA1B.		
OS	Mesocricetus auratus (Golden hamster).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;		
OC	Mesocricetus.		
OX	NCBI_TaxID=10036;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89017157; PubMed=2845398;		
RA	Cotecchia S., Schwinn D.A., Randall R.R., Lefkowitz R.J.,		
RA	Caron M.G., Kobilka B.K.;		
RT	"Molecular cloning and expression of the cDNA for the hamster alpha		
RT	1-adrenergic receptor.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 85:7159-7163(1988).		
RN	[2]		
RP	MUTAGENESIS OF ALA-293.		
RX	MEDLINE=92112850; PubMed=1346134;		
RA	Kjelsberg M.A., Cotecchia S., Ostrowski J., Caron M.G.,		
RA	Lefkowitz R.J.;		
RT	"Constitutive activation of the alpha 1B-adrenergic receptor by all		
RT	amino acid substitutions at a single site. Evidence for a region		
RT	which constrains receptor activation.";		
RL	J. Biol. Chem. 267:1430-1433(1992).		
CC	-!- FUNCTION: This alpha-adrenergic receptor mediates its action by		
CC	association with G proteins that activate a phosphatidylinositol-		
CC	calcium second messenger system.		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
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CC	or send an email to license@isb-sib.ch).		
DR	EMBL; J04084; AAA58964.1; --		
DR	PIR; A0491; A40491.		
DR	HSP; P29274; LMWH.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRHHODOPSN.		
DR	PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.		
DR	PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;		
KW	Multigene family; Phosphorylation; Lipoprotein; Palmitate.		
FT	DOMAIN 1 45		
FT	TRANSMEM 46 70		
FT	DOMAIN 71 83		
FT	TRANSMEM 84 105		
FT	DOMAIN 106 115		
FT	TRANSMEM 116 141		
FT	DOMAIN 142 161		
FT	TRANSMEM 162 182		
FT	DOMAIN 183 201		
FT	TRANSMEM 202 224		
FT	DOMAIN 225 295		

```

FT TRANSMEM 296 319 6 (POTENTIAL).
FT DOMAIN 320 326 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 327 340 7 (POTENTIAL).
FT TRANSMEM 341 345 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 371 378 POLY-ARG.
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 118 195 BY SIMILARITY.
FT LIPID 365 365 S-palmitoyl cysteine (Potential).
FT MUTAGEN 293 293 A->X; CONFPERS CONSTITUTIVE ACTIVITY.
SQ SEQUENCE 515 AA; 56492 MW; 6DAF1576D1C1CE2D CRC64;

Query Match 14.1%; Score 288.5; DB 1; Length 515;
Best Local Similarity 25.1%; Pred. No. 11e-12;
Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCVHE-----SVLGKRYV--AVSGWVVA---VTGTVGNVLTLLALAIQPKL 51
DB 17 WGEIKDANFTGPNQTSNSTLPQLDVTFAISVGLVGAFLFAIVGNILVILSVACNHL 76
QY 52 RTRFNLLIANLTADLLLYTLLQPSVDVYLHLHWRGATFCRVFGLLLFASNSVSLTL 111
DB 77 RPTNYFIWLAIALDLLLSFTLPFSATLEVGLYWLGRIFCDIWAADVVLCTASILSL 136
QY 112 CLIALGRYLLAHKPLFPQVFSKAGIVLALVSTWVG-VASFAPL--WPIYILVPVVC 168
DB 137 CAISIDRIVGVRSLOYPQLVTRRAILALSVWLSTVISIGPLLGK-----EPAPND 192
QY 169 SFDIRGRPYTILMGI-YFVLGSSVGIFCYLIHROVKRAAALDOYKLRQASIHSHV 227
DB 193 KEGGVTEPFYALFSSLSGFYPLAVILWYCRVIVAKRTTKNLEAGVMKES----- 246
QY 228 ARTEAMPGRQELDRLASGPGSEGISSEPVSAATTQLEGDSSEVDQINSKRAQMA 287
DB 247 -----NSKELTLRIHSKNFHE-----DTLSSTKAK--- 271
QY 288 EKSPPEASAKQPIKGARRAPDSSEFGKTRMCFVFLCFALSIYIFLL--LNILDA 344
DB 272 -GHNPRSSIAVKLFKFSRE-KKAATLGIUVGM-----FILCWLFFPALPLGSLFST 322
QY 345 VOARVVMHLAANTWLVNGCINPVLYAMNRPQVAGSILKRGPRFHR 394
DB 323 LKPPDAVKVFWLGYFNCLNPFIYPCSKKEFKRAFMRLGCOCRSGRR 372

RESULT 8
D2DR_BOVIN STANDARD; PRT; 444 AA.
AC P20288;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE D(2) dopamine receptor.
GN DR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RA MEDLINE=90136899; PubMed=2137198;
RA Chio C.L., Hess G.F., Graham R.S., Huff R.M.;
RT "A second molecular form of D2 dopamine receptor in rat and bovine
RL Nature 343:266-269 (1990).
CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors
CC for dopamine. The activity of this receptor is mediated by G
CC proteins which inhibit adenylyl cyclase.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;

```

```

CC CC Name=Long;
CC CC IsoID=P20288-1; Sequence=Displayed;
CC CC Name=Short;
CC CC IsoID=P20288-2; Sequence=VSP 001869;
CC CC -!- SIMILARITY: Belongs to family I of G-protein coupled receptors.
CC -----
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CC -----
CC CC EMBL; X51657; CAA35970.1; -
CC CC F1R; S08163; DYBOD2.
CC CC InterPro; IPR000276; GPCR_Rhodpsn.
CC CC Pfam; PF00001; 7tm.1; 1.
CC CC PRINTS; PR00237; GPCRHOOPS.
CC CC PROSITE; PS00237; G-PROTEIN RECF_1_1; 1.
CC CC PROSITE; PS00262; G-PROTEIN RECF_1_2; 1.
CC CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Alternative splicing.
CC CC DOMAIN 1 37
CC CC EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 38 60 1 (POTENTIAL).
CC FT DOMAIN 61 71 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 72 97 2 (POTENTIAL).
CC FT DOMAIN 98 108 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 109 130 3 (POTENTIAL).
CC FT DOMAIN 131 151 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 152 174 4 (POTENTIAL).
CC FT DOMAIN 175 186 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 187 210 5 (POTENTIAL).
CC FT DOMAIN 211 374 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 375 398 6 (POTENTIAL).
CC FT DOMAIN 399 406 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 407 430 7 (POTENTIAL).
CC FT DOMAIN 431 444 CYTOPLASMIC (POTENTIAL).
CC FT SITE 193 193 IMPLICATED IN CATECHOL AGONIST BINDING
CC FT SITE 194 194 (BY SIMILARITY).
CC FT SITE 194 194 IMPLICATED IN RECEPTOR ACTIVATION
CC FT SITE 197 197 (BY SIMILARITY).
CC FT SITE 197 197 IMPLICATED IN RECEPTOR ACTIVATION
CC FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT DISULFID 107 182 BY SIMILARITY.
CC FT VARSPLIC 242 270 Missing (in isoform Short).
CC FT SEQUENCE 444 AA; 50671 MW; 67437197629301C7 CRC64;
CC -----
CC CC Query Match 14.1%; Score 288; DB 1; Length 444;
CC CC Best Local Similarity 26.8%; Pred. No. 1e-12;
CC CC Matches 112; Conservative 65; Mismatches 181; Indels 60; Gaps 14;
CC -----
CC QY 19 YRYVAVSGVAVVAVTGVGNVLTLLALAIQPKLRTFRNLLIANLTADLLYCTLLQPSV 78
CC DB 34 YNYVAMLLTLTIFVTI-VFNGVLVCNAVSRERKALQTTNNYLVSLAVADLLVATLMPVW 92
CC QY 79 DTYLHL--HWRTGATFCRVFGLLLFASNSVSLTCLIALGRYLLIAHPKLPQVFSAGK 136
CC DB 93 --YLEVGVGEKFSRIHCDIFVTLDVMCTASILNLCASIDRYTAVAMPMLNTRYSKR 150
CC QY 137 IVALLVSTWVGVASFAELWPIYILVPVVCVCSFDRINGRPTTILMGI-----YFVLG 190
CC DB 151 RVTVMA--IVWLSFTISCP--MLFGLNLDQNECIANPAFVYSSIVSYFVPFVTL 206
CC QY 191 LSSGVFCYLIHQ-----VKRAAQL-----DOYKLRQASHSN---HVA 228
CC DB 207 LVYIKIYIVLRRRRKRVNTRKSSAFRANLKAFLKGNCTHPEDMKLCTVIMKNSGSPVN 266
CC QY 229 RTDEAMPGRFOELD-SRLASGPGSEGISSEPVSAATTQLEGDSSEVG----- 275

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Db 267 RRAVEARRAQAEMEMLSSTSPERTVSPPIPPSHQLTLPDPSSHGLHSTPDSAPKE 326
QY 276 -----DOINSKRAQKWAESPASAKAOPKARRAPSSSEFGKVTMCRFAVLCFAL 330
Db 327 KNGHAKTVNPKIAKIFEIQMNGKTKTS-LKTMRSRKLSQCKEKATQMLAIVLGVFI 385
QY 331 SYIPFLNLNILDARVOAPRVVHMLAANLTLWL---NGCINPVLVYAMNRQFRQAYGSIL 385
Db 386 CWLPPFTIHLNHCDC-NIPPVLYSAFTWLVGVSNAVPIITTFNIEPRKAFKLIL 442
RESULT 9
ALAB RAT
ID ALAB RAT STANDARD; PRT; 515 AA.
AC P15823; Q63215;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).
GN ADRA1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=90192094; PubMed=2156222;
RA Voigt M.M., Kispert J., Chin H.;
RT "Sequence of a rat brain cDNA encoding an alpha-1B adrenergic
receptor.";
RL Nucleic Acids Res. 18:1053-1053 (1990).
RN [2]
RC SEQUENCE FROM N.A.
RP MEDLINE=9117789; PubMed=1706716;
RA Lomasney J.W., Cotecchia S., Lorenz W., Leung W.-Y., Schwinn D.A.,
RA Yang-Peng T.L., Brownstein M., Lefkowitz R.J., Caron M.G.;
RT "Molecular cloning and expression of the cDNA for the alpha 1B-
adrenergic receptor. The gene for which is located on human
chromosome 5.";
RL J. Biol. Chem. 266:6365-6369 (1991).
RN [3]
RC SEQUENCE FROM N.A.
RP MEDLINE=94010315; PubMed=9406017;
RA Gao B., Xunos G.;
RT "Isolation and characterization of the gene encoding the rat alpha 1B
adrenergic receptor.";
RL Gene 131:243-247 (1993).
RN [4]
RC SEQUENCE OF 1-253 FROM N.A.
RP MEDLINE=95081407; PubMed=7989580;
RA Kanasaki M., Matsubara H., Murasawa S., Masaki H., Nio Y., Inada M.;
RT "cAMP responsive element-mediated regulation of the gene
transcription of the alpha 1B adrenergic receptor by thyrotropin.";
RL J. Clin. Invest. 94:2245-2254 (1994).
CC -!- FUNCTION: This alpha-adrenergic receptor mediates its action by
association with G proteins that activate a phosphatidylinositol-
calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; X51585; CAA35934.1; -;
DR EMBL; M60655; AAA63478.1; -;
DR EMBL; L08610; AAA40647.1; -;

EMBL; L08609; AAA40647.1; JOINED.
DR EMBL; D32045; BAA06806.1; -;
DR PIR; JC1525; JC1525.
DR HSSP; P29274; 1NMH.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECF F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Palmitate.
KW Multi-gene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 45
FT TRANSMEM 46 70
FT DOMAIN 71 83
FT TRANSMEM 84 105
FT DOMAIN 106 115
FT TRANSMEM 116 141
FT DOMAIN 142 161
FT TRANSMEM 162 182
FT DOMAIN 183 201
FT TRANSMEM 202 224
FT DOMAIN 225 235
FT TRANSMEM 236 295
FT DOMAIN 296 319
FT TRANSMEM 320 326
FT TRANSMEM 327 340
FT DOMAIN 341 515
FT TRANSMEM 371 378
FT CARBOHYD 10 10
FT CARBOHYD 24 24
FT CARBOHYD 34 34
FT DISULFID 118 195
FT LIPID 365 365
FT CONFLICT 114 116
FT CONFLICT 203 203
FT CONFLICT 207 207
FT CONFLICT 306 306
FT CONFLICT 415 416
FT CONFLICT 440 440
FT CONFLICT 484 486
FT CONFLICT 493 493
FT CONFLICT 511 511
SQ SEQUENCE 515 AA; 56585 MW; AF0C3759F80C3135 CRC64;
Query Match 14.1%; Score 287.5; DB 1; Length 515;
Best Local Similarity 24.9%; Pred. No. 1.3e-12;
Matches 96; Conservative 71; Mismatches 15; Indels 67; Gaps 12;
QY 23 AVSWGQVVA---VTGTGNGVLTALALAIQPKLRTFRNLLIANLTLADLLYCTLLQPPSVD 79
Db 45 AISVGLVGAFLFAIVGNILVILSVACNRHLRPTNYFIVNLATADLLLSFTVLPFSAT 104
QY 80 TYLHLHWRGTGATFCRVFGLLPASNSVSLTCLIALGRVLLIAHPKLPQVFSAKGVIL 139
Db 105 LEVLGYNVLRGIFCDIWAADVLCCTASILSCALSIDRYIGVYSLOYPLVTRKAIL 164
QY 140 ALVSTVWVG-VASAPL--WPIYILVPPVCTSPDRIRGRPYTILMGI-YFVLGLSSVG 195
Db 165 ALLSVVLSTVLSIGFLGWK---EPAPNDKCEGVTEEPYALFSSLSGFYIPLAVIL 220
QY 196 IFYCLHQRVKAQALDQYKLRQASIHNSHVARTDEAMPGRFQELDSLASGGSEGIS 255
Db 221 VMYCRVYIVAKRTTKNLEAGVKNEMS-----NSKELTURIKSNFHE--- 262
QY 256 SEPVSAAATQTLGDSSEVQINSKRAQKWAESPASAKAOPKARRAPSSSEFG 315
Db 263 -----DTLSSTKAK---GHNPSIAVKLFKESRE-KKAATKLG 297
QY 316 KVTMCRFAVLCFALSYLTPFL---LNILDRVQAPRVVHMLAANLTLWNGCINPVLAA 372
Db 298 IVVGM-----FILCWLPFFIALPLGLSTLKPDAVFKVFWLGFNSCLNPIIYPC 350
QY 373 MNRQFRQAYGSILK---RGRPSFHR 394

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SQ      SEQUENCE      443 AA;  50590 MW;  34165B56460B524D CRC64;

Query Match      14.1%;  Score 287;  DB 1;  Length 443;
Best Local Similarity 25.6%;  Pred. No. 1.2e-12;
Matches 113;  Conservative 66;  Mismatches 183;  Indels 80;  Gaps 15;

QY      2  WNSDANPSCVHESVLGRVYVAVSWGVAVTGCVNLTLALAIQPKLRTFNLIAN 61
DB      22  FNGSGKADRH-----YNYATLLTLLIAYI-VFGNVLVCMVSEKALQTTNYLIVS 75

QY      62  LTLADLLYCTLLQPSVDYTLHL--HWRTGATFCRVFGLLFPASNSVILTLCLIALGRY 119
DB      76  LAVADLLVATLWMPWVV--YLEVVGEWKFSKIHCDIFVTLDVMMCTASILNLCASIDRY 133

QY      120  LLIAPKLFQGVFSAKGIVLALYSTWVGVGASAPLWPIYILVPVVTCTSPDRIRGRPYT 179
DB      134  TAVAVPMLYNTNRYTSKRRTVMIA--IVWVLGFT-----ISCPLLFGLNNAQNE 181

QY      180  TILMGIYFVLGLSGVGIF-----YCLIHQ-----VKRAAQAL----- 212
DB      182  CIANPAFVYSSIVFVPIVTLVVIKIVLRRRKRYNTRKSEAPRSHLRAPLK 241

QY      213  -----DOYKLRQASIHNN---HWATDEAMPGRQELD-SRLASGGSEGISSEPIVSA 262
DB      242  GNCTHPEDMKLCTVIMKSNGSFFNRRRYVEAARRAQAELEMEMLSLTSPPERTRYSP 301

QY      263  TTOTLEGDSSEVG-----DOINSKRAQMAEKSPPEASAKAQPIKGARR 306
DB      302  HQHQLTLPDPSHHGLHSTPDSAPKXNGHAKQHPKIAKIFELQTPNGKRTS-LKTM 360

QY      307  APDSSSEFGKTRMCFVAVLCFALSYPILLNLINDARVQAPRVVHMLAANLTWL--NG 363
DB      361  RKLSQLQEKKATQMLAIVLGVFICLIPFFFIITHILNIHDCD-NIPPVLYSAFTW 419

QY      364  CINPVLYAANNRQFRQAYGSIL 385
DB      420  AVNPFIYTFNIEFRKAFKLIL 441

RESULT 11
ALAB_HUMAN
ID      ALAB_HUMAN      STANDARD;      PRT;      519 AA.

AC      F35368;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).
DE      ADRA1B
GN      GN
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_TaxID=9606;
RN      [1]_
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93016158; PubMed=1328250;
RA      Ramarao C.S.; Denker J.M.; Perez D.M.; Gaivin R.J.; Riek R.P.;
RA      Graham R.M.;
RT      "Genomic organization and expression of the human alpha 1B-adrenergic
RT      receptor.";
RL      J. Biol. Chem. 267:21936-21945(1992).
RN      [2]_
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=94233986; PubMed=9183249;
RA      Forray C.; Bard J.A.; Wetzel J.M.; Chiu G.; Shapiro E.; Tang R.;
RA      Lepor H.; Hattig P.R.; Weinschank R.L.; Branchek T.A.;
RA      Gluchowski C.;
RT      "The alpha 1-adrenergic receptor that mediates smooth muscle
RT      contraction in human prostate has the pharmacological properties of
RT      the cloned human alpha 1C subtype.";
RL      Mol. Pharmacol. 45:703-708(1994).
RN      [3]_
RP      SEQUENCE FROM N.A.

```


Db 22 FNGSEKADPH:---YNYVAMLLTLIIPII-VFNGVLVCMVAVSREKALQTTTNIIVS 75
 Qy 62 LTLADLLYCTLLQPFSDVTLHL--HWRTGATCRVFGLLLFASNSVSLTLCIALGRY 119
 Db 76 LAVADLLVAPLVMPWV--YLEVVGWKKFSRIHCDIFVTLDVNMCTASINLCASIDRY 133
 Qy 120 LLIAHPKLPQVFSAGKIVLALVS-TWVGVGASFAPLMPIIYILVVPVCTCSFDRIRGRY 178
 Db 134 TAVAMPMLNYTRYSSKRRVTMTAIVWLSFTISCLP-----LFGLNNDQNECIITANPA 188
 Qy 179 TTILMGI-----YFVLGLSSGVIIFYCLIHQ-----VKRAAQL-----D 213
 Db 189 FVYSSIVSFYVPIVTLIIYIYIVLRKRRKRVNTKSSRAFRANLKTPLKGNCTHPE 248
 Qy 214 QYKLRQASIHNS-----HVARTEAMPGRFOELD-SRLASGGPSEGISEPVSAATQTL 267
 Db 249 DMKLCVTIMKNSGFPVWRMRMDAAR--RAQELMEMXLSSTSPETRTVSPFPSSHQLT 306
 Qy 268 EGDSSVVG-----DQINSKRAQMAEKSPPEASAKAPIOIKGARAPDS 310
 Db 307 LPDPSSHGLHSNPDSPAKPEKNGHAKIVNPRIAKFPEIQTMPNGKTRTS-LKTMSSRKLS 365
 Qy 311 SSFEGKVTMCFPVFLCFALSYPILLNLIDARVQAPRVVHMLAANLTWL---NGCINP 367
 Db 366 QQEKKATQMLAIVLGVFIICWLPFFITHILNIHDCD-NIPPVLYSAFTWLGTVNSAVRP 424
 Qy 368 VLYAAMNRQFQAYGSIL 385
 Db 425 IIVTTNIEBKAFMKIL 442

RESULT 13
 ID AIAA BOVIN STANDARD; PRT; 466 AA.
 AC P18130;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
 DE adrenergic receptor).
 GN ADRA1A OR ADRA1C.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90243698; PubMed=1970822;
 RA Schwinn D.A., Lomasney J.W., Lorenz W., Szklut P.J., Fremean R.T. Jr.,
 RA Yang-Feng T.L., Caron M.G., Lefkowitz R.J., Cotecchia S.;
 RT "Molecular cloning and expression of the cDNA for a novel alpha 1-
 RT adrenergic receptor subtype."
 RL J. Biol. Chem. 265:8183-8189(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92087349; PubMed=1966743;
 RA Schwinn D.A., Cotecchia S., Lorenz W., Caron M.G., Lefkowitz R.J.;
 RT "The alpha 1C-adrenergic receptor: a new member in the alpha 1-
 RT adrenergic receptor family."
 RL Trans. Assoc. Am. Physicians 103:112-118(1990).
 CC -1- FUNCTION: This alpha-adrenergic receptor mediates its action by
 CC association with G proteins that activate a phosphatidylinositol-
 CC calcium second messenger system. Its effect is mediated by G(q
 CC and G(11) proteins.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; J05426; AAA30374.1; -;
 CC PIR; A35375; A35375.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm1.1;
 CC PRINTS; PR00237; GPCRHOPOPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECP_F2_1; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Palmitate.
 CC Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 CC EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 1 27
 CC TRANSMEM 28 51
 CC DOMAIN 52 64
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 65 88
 CC DOMAIN 89 99
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 100 122
 CC DOMAIN 123 143
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 144 167
 CC DOMAIN 168 181
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 182 205
 CC DOMAIN 206 273
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 274 297
 CC DOMAIN 298 305
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 306 329
 CC DOMAIN 330 466
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 467 480
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC TRANSMEM 481 515
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC TRANSMEM 516 545
 CC PHOSPHORYLATION (BY PKA) (POTENTIAL).
 CC TRANSMEM 546 575
 CC BY SIMILARITY.
 CC TRANSMEM 576 585
 CC S-palmitoyl cysteine (Potential).
 CC TRANSMEM 586 595
 CC SEQUENCE 466 AA; 51466 MW; 77635153B39B85EC CRC64;
 Query Match 13.8%; Score 281.5; DB 1; Length 466;
 Best Local Similarity 23.0%; Pred. No.2.9e-12;
 Matches 95; Conservative 82; Mismatches 153; Indels 83; Gaps 13;
 Qy 3 NSSDANFCYHESVLYGRIYAVSGVVVA---VTGTGVGNVLTLLALAIQPKLRFNLLI 59
 Db 7 NASDSS-NCTHPPPPVNTSKAILGLVGLGLILFGLVGNILVILSVACHRLHSVTHYVI 65
 Qy 60 ANLTADLLYCTLLQPFSDVTLHLHWRTGATCRVFGLLLFASNSVSLTLCIALGRY 119
 Db 66 VNLAVADLLTSTVLPFSAIFEILGYWAFGRVFCNVMAAVDVLCCTASIMGLIISIDRY 125
 Qy 120 LLIAHPKLPQVFSAGKIVLALVSTWVVG-VASAPLMPYIYILVP---VWCTCSFDRIRG 175
 Db 126 IGVSYPYLPYIVTQKRGMLLCVWALSIVISIGPLFGWQPAPEDETIC-----QINE 180
 Qy 176 RPYTILMGI-YFVLGLSSGVIIFYCLIHQVKRAAQLDQYKLRQASIHSHVARTDEAM 234
 Db 181 EFGYVLFSAIGSFYVPLTIILVMYCRVTVVAVKRSRGL----- 218
 Qy 235 PGRFQELDSRLASGGPSEGISEPVSAATTTQLEGDSSEVGQINSKRAQMAEKSPPEA 294
 Db 219 -----KSGLXTD-----KSDSQVTLRHKNA-QVGGSGVTS 251
 Qy 295 SAX-----AQPIKGARRAPDSSEFGKVTMCFVFLCFAISYIPPLLNLIDA----RVQA 347
 Db 252 KNTKTHFSVRLKFSREK-----KAAKTLGIVGVCFVLCWLPPLFPFLVPIGSPFDFRP 303
 Qy 348 PRVTHMLAANLTWNGCINPVLVYAMNFEQRAQVSI-----LKGPRSSFHL 395
 Db 304 SETVFKAIFWLGYNLCINPIIYPCSOEKKAFQNVLRIOCLRRKQSKHTL 356

RESULT 14
 OAE2 LOCM1
 ID OAE2 LOCM1 STANDARD; PRT; 484 AA.
 AC Q25322;

15-JUL-1998 (Rel. 36, Created)
 15-JUL-1998 (Rel. 36, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Putative tyramine receptor 2 (Tyrl-Loc2).
 GN GCR2.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.
 CX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neuron;
 RA Vanden Broeck J.J.M.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: G-protein coupled receptor for tyramine, a known
 CC neurotransmitter and neuromodulator and direct precursor of
 CC octopamine (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC -----
 DR EMBL; X69521; CAA49269.1; -;
 DR HSSP; P29274; IMMH.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1.1;
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 54
 FT TRANSMEM 55 77
 FT DOMAIN 78 87
 FT TRANSMEM 88 109
 FT DOMAIN 110 126
 FT TRANSMEM 127 147
 FT DOMAIN 148 167
 FT TRANSMEM 168 190
 FT DOMAIN 191 215
 FT TRANSMEM 216 237
 FT DOMAIN 238 411
 FT TRANSMEM 412 433
 FT DOMAIN 434 448
 FT TRANSMEM 449 470
 FT DOMAIN 471 484
 FT CARBOHYD 13 13
 FT CARBOHYD 198 198
 FT DISULFID 124 203
 FT DOMAIN 286 292
 FT DOMAIN 294 307
 FT DOMAIN 348 360
 FT TRANSMEM 361 385
 SQ SEQUENCE 484 AA; 53488 MW; 15C10608471D77CD CRC64;
 Query Match 13.8%; Score 281; DB 1; Length 484;
 Best Local Similarity 24.5%; Pred. No. 3.3e-12;
 Matches 111; Conservative 63; Mismatches 187; Indels 92; Gaps 17;
 15 SVLGKRYVAVSGWVAVTG-----TGVNLTLLALAIQKLRFRNLLIANLTAD 66
 38 SVLGKRYVAVSGWVAVTG-----TGVNLTLLALAIQKLRFRNLLIANLTAD 97
 67 LLYCTLLQPSGVDTYHLHRTGATCRVGLLLFASNSVSLTCLIALGRYLLIAHPK 126
 98 LTVAVLVNPFNVAVSLQKRVGIVGVCKMWTCDVLCCTASILNLCALADRTHWTDPI 157
 127 LFPQVFSAGKIVTALVSTWVY-GVASFAPL-----WPIYI--LVFVYVCTCSFDRIRGRPY 178

Db 158 NYAQRTRRVVLAMTAGVWLLSGVSSPPLIGWDMFENFTTP-----COLTEQGVYI 213
 QY 179 FTILMGYI---FVLGLSSVGIFYCLIHQVKRAA-----QALDQYKLRQA----- 220
 Db 214 YSLGSPFIPILFIMTVYVEFIATKRLRERAKSKLNSAMKQMAAQAVPSSVPSHDQ 273
 QY 221 ---STHSNH-----VATDEAMPGRF-----QELDSRLAS 247
 Db 274 EVSSETNHNELPPPPAPSPSEKRRKTKKKKKQQAEEGRFLAPAMVAEDSVTDNSVS 333
 QY 248 GGF--SEGISSEPVSAATOTLEGDSSEVGQINSKRAKQMAEKSP--EASAKAQP----- 300
 Db 334 VGVPAKNHLAEDGYTCTTTTITTTTAVTDSRSRTASQKSTAPTPVQPKSIPVYQF 393
 QY 301 IKGARRAPDSSEFGKVTMCFAYPLCFALSYIFLLNLIL-----DARVQAPRVHMLA 355
 Db 394 IBEKQRI--SLSKERRAARTLGIINGVFCWLVFFLMYIVPFCNPCKSPKLVNF-- 449
 QY 356 ANLTWL---NGCINPVLVYAMNRPQAYGSIL 385
 Db 450 --ITWLGVINSALNPILYITFNLPERRAFKXLL 480
 RESULT 15
 OARI_LOCM1
 ID OARI_LOCM1 STANDARD; PRT; 484 AA.
 AC Q25321.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tyramine receptor 1 (Tyrl-Loc1).
 GN GCR1.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.
 CX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC TISSUE=Neuron;
 RC MEDLINE=95279566; PubMed=7760020;
 RA Vanden Broeck J.J.M., Vultsteke V., Huybrechts R., de Loof A.;
 RT "Characterization of a cloned locust tyramine receptor cDNA by
 RT functional expression in permanently transformed Drosophila S2
 RT cells.";
 RL J. Neurochem. 64:2387-2395(1995).
 CC -!- FUNCTION: G-protein coupled receptor for tyramine, a known
 CC neurotransmitter and neuromodulator and direct precursor of
 CC octopamine. The rank order of potency for agonists of this
 CC receptor is tyramine > naphazoline > tolazoline > DL-octopamine >
 CC dopamine > epinephrine > 5-hydroxytryptamine. For antagonists, the
 CC rank order is yohimbine > chlorpromazine > mianserin >
 CC phentolamine > metoclopramide.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Present mainly in the central nervous system,
 CC especially in the supra- and suboesophageal, thoracic and
 CC abdominal ganglia. Not found in the distal part of optic lobes.
 CC -!- DEVELOPMENTAL STAGE: Expressed in the nervous system by the
 CC first larval stage.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL; X69520; CAA49268.1; -;
 DR FIR; S58868; S58868.
 DR HSSP; P29274; IMMH.


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DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G PROTEIN RECP F1 1; 1.
DR PROSITE; PS00262; G PROTEIN RECP F1 2; 1.
DR PROSITE; PS00262; G PROTEIN RECP F1 3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 55 77 1 (POTENTIAL).
FT DOMAIN 78 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 167 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 168 190 4 (POTENTIAL).
FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 237 5 (POTENTIAL).
FT DOMAIN 238 411 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 412 433 6 (POTENTIAL).
FT DOMAIN 434 448 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 449 470 7 (POTENTIAL).
FT DOMAIN 471 484 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 124 203 BY SIMILARITY.
FT DOMAIN 286 292 POLY-PRO.
FT DOMAIN 294 307 ARG/LYS-RICH (BASIC).
FT DOMAIN 348 360 POLY-THR.
SQ SEQUENCE 484 AA; 53530 MW; 4484FBC85A810619 CRC64;

Query Match
Best Local Similarity 13.7%; Score 280; DB 1; Length 484;
Matches 111; Conservative 63; Mismatches 187; Indels 92; Gaps 17;

QY 15 SVLGRYVAVSWGVAVTG-----TVGNVLTLLALAIQPKLRNLLIANLTAD 66
DB 38 SVLGRLVAPENEVAVTAVSLIIILITVGNVLVLSVFTYKPLRIVQNFIVSLAVAD 97
QY 67 LLYCTLLQPFVPTYLHLHRTGATCRVEGLLFFASNSVSLTCLIALGRYLLIAHPK 126
DB 98 LTAVLVMPFNVAISLIQRVFGIVCKWLTCDVLCCTASILNLCAIALDRYWAITDPI 157
QY 127 LFPQVFSAGIVLALYSTVWV-GVASFAPL-----WPIYI--LVPVVTCSFDRINGRPY 178
DB 158 NYAQKTLRRVLAMIAGVLLSGVISPPPLIGNWDWNEFNDTP-----CQLTEEGYVI 213
QY 179 TTILMGYI---FVLGLSSGIFYCLTHROVKRAA-----QALDQYKLQA----- 220
DB 214 YSSLSGFFPIFLFMTIVYVEIFATKRLERAKASKLNSAMKQQAQAAVSSVPSHDQ 273
QY 221 ---SIHNSH-----VARTDEAMGGRF-----QELDSRLAS 247
DB 274 ESVSSETNHNELPPPPAPPSPKERRKTKKKKKQAEEGREFLAPAMVAEDSVTDNSVS 333
QY 248 GGP--SEGISSEFVAATTTOTLEGDSSEVDQINSKRAKMAEKSPPEASAKAQP---- 300
DB 334 VGPVARNHLAEDGYCTTTTITTTTAVTDSRSTASCKGSTAPPTVPQKSIPIYQF 393
QY 301 IKGARAPDSSSEFGKVRNCFVFLCFALSYIPFLNLIL-----DARVQAPRVVHMLA 355
DB 394 IEEKQRI--SLSKERRAARTLGIIMGVGVVWLPFFLWVIVFVFCNPKSPCKPLVNF-- 449
QY 356 ANLTWL---NGCINPVLVYAMNPFQAYGSIL 385
DB 450 --ITWLGINSALNPIIYITFNLDFFRAFKLL 480

Search completed: September 24, 2004, 08:37:06
Job time : 26 secs
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DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 396 AA; 43717 MW; 80F0601CBB4B1B03 CRC64;

Query Match 85.7%; Score 1749; DB 11; Length 396;
Best Local Similarity 85.6%; Pred. No. 5.2e-138;
Matches 339; Conservative 19; Mismatches 38; Indels 0; Gaps 0

QY 1 MNNSDANFSCYHESVLCGRYVAISWGVAATCTGVNLTLLALAIQPKLRFNLLIA 60
DB 1 MNNSDANFSCYHESVLCGRYFAVINGVAVATCTGVNLTLLALAIQPKLRFNLLIA 60
QY 61 NLTLADLYCTLLQPFSDVDTLHLHWTGATFCRVFGLLPFASNSVSIITLCIALGRYL 120
DB 61 NLTLADLYCTLLQPFSDVDTLHLHWTGAVFCRI FGLLFTSNSVSIITLCIALGRYL 120
QY 121 LIAHPKLFPQVFSKAGIYALIVSTVVVGVSFAFLMPYIYLVVCTCGFDRIRGRPYTT 180
DB 121 LIAHPKLFPQVFSKAGIYALVGSWVGVTSFAPLMNVFLVPVCTCGFDRMRGRPYTT 180
QY 181 ILMGIYFVLGSSVGIIFYCLIHROVKRAAALDOYKLROASIHSHVARTDEAMPGRFOE 240
DB 181 ILMGIYFVLGSSVGVFVCLIHROVKRAAALDOYGLHQASISHQVAGTQEAHPGRFOE 240
QY 241 LBSRLASGPGSEGISSEFVSAATQTLEGDSSEVGDOINSKRAKQMAEKSPPESAQAOP 300
DB 241 LDSGVASRGPSEGISSEFVSAATQTLEGDSSEAGGQIRKAAQIAERSLPEVHRKPRE 300
QY 301 IKGARRADPSSERFGKTRMCFVFLCFALSYIPFLNLINILTDARVOAPRVVHVAANLTW 360
DB 301 TAGARRATDPSERFGKTRMCFVFLCFALSYIPFLNLINILTDARGRAPRVVHVAANLTW 360
QY 361 LNCINPVLVYAMNRPQACVGSILKEGPRSFURLH 396
DB 361 LNSCINPVLVYAMNRPQFHVAGSILKEGQPSFRFHH 396

RESULT 3
Q99MX9 PRELIMINARY; PRT; 396 AA.
ID Q99MX9
AC Q99MX9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Orphan G protein-coupled receptor 84.
GN GPR84.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RC MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellebrand S.;
RT an expressed sequence tag (est) data mining strategy succeeding in
RL the discovery of new G-protein coupled receptors.";
RL J. Mol. Biol. 307:799-813(2001).
DR EMBL; AF272948; AAK01859.1;
DR MGD; MG1:1934129; Gpr84.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1;
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 396 AA; 43731 MW; D7536A2FE96462D8 CRC64;

Query Match 85.6%; Score 1749; DB 11; Length 396;
Best Local Similarity 85.4%; Pred. No. 6.3e-138;

		Matches	338;	Conservative	20;	Mismatches	38;	Indels	0;	Gaps	0;
QY	1	MNNSDANTSCYHESVGLGYYAVSVGVVAVTGTGVTGNTLLALAIQPKLRTFNLLIA	60								
DB	1	MNNSDANTSCYHESVGLGYYAVSVGVVAVTGTGVTGNTLLALAIQPKLRTFNLLIA	60								
QY	61	NLTADLLYCTLLQPSVDYTLHLHWRGTGATFCRVFGLLIFASNSVSIITLCIALGRYL	120								
DB	61	NLTADLLYCTLLQPSVDYTLHLHWRGTGATFCRVFGLLIFASNSVSIITLCIALGRYL	120								
QY	121	LIHAPKLPFQVFAKGIIVALVSTWVGVASFAPIWPIVILYVVTCTCFDIRGRPYTT	180								
DB	121	LIHAPKLPFQVFAKGIIVALVSTWVGVASFAPIWPIVILYVVTCTCFDIRGRPYTT	180								
QY	181	ILMGIVFVLGLSVGIFCYCLIRHOVKRAAALQYKLRQASHNSHVARTDEAMPQRFQ	240								
DB	181	ILMGIVFVLGLSVGIFCYCLIRHOVKRAAALQYKLRQASHNSHVARTDEAMPQRFQ	240								
QY	241	LDLRLASGSPSEGISSEPVSAATQTLEGDSSEVGQINSKRAKQWAEKSPFASAKAP	300								
DB	241	LDLRLASGSPSEGISSEPVSAATQTLEGDSSEVGQINSKRAKQWAEKSPFASAKAP	300								
QY	301	IKGARAPDSSSEFGKTRMCFVAVLFCFALSYIPFLLNILDARVOAPRVHMLAANLTW	360								
DB	301	IKGARAPDSSSEFGKTRMCFVAVLFCFALSYIPFLLNILDARVOAPRVHMLAANLTW	360								
QY	361	LNGCINPVLVYAMNRFQRAYGSLKRGPSFRHLH	396								
DB	361	LNSCINPVLVYAMNRFQRAYGSLKRGPSFRFH	396								
RESULT 4											
QW534	PRELIMINARY; PRT; 670 AA.										
AC	QW534; 2000 (TrEMBLrel. 13, Created)										
DT	01-MAY-2002 (TrEMBLrel. 22, Last sequence update)										
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)										
DE	CG4322 protein.										
GN	EG:22E5.11 OR CG4322.										
OS	Drosophila melanogaster (Fruit fly).										
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;										
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;										
OC	Ephydroidea; Drosophilidae; Drosophila.										
OX	NCBI_TaxID=7227;										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RC	STRAIN=Berkely;										
RX	MEDLINE=20196006; PubMed=10731132;										
RA	Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,										
RA	Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,										
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,										
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,										
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,										
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,										
RA	Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,										
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Baasley E.M.,										
RA	Beeson K.Y., Benos P.V., Berman B.P., Shandari D., Bolshakov S.,										
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,										
RA	Burtis J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,										
RA	Cherry J.M., Cadieu E., Center A., Cadieu E., Center A., Chandra I.,										
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,										
RA	Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,										
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,										
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,										
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,										
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,										
RA	Hoskins R.A., Howland T.J., Wei M.-H., Ibegwan C.,										
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,										
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,										
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,										
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.F., McPherson D.,										
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,										

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster";
Science 287:2185-2195(2000).
[2]
SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Barson J., An H., Baldwin D., Banon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Dou L.E., Doyle C., Dresnek D., Farfan D.,
Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
Pacle J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
Shouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of Drosophila melanogaster genome";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradsky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
Tup J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smurniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
"Annotation of Drosophila melanogaster genome";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB003422; AAF45709.2; -;
DR FlyBase; FBgn0025631; EG:22E5.11.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 670 AA; 71932 MW; 90B894941A366546 CRC64;
Query Match 18.5%; Score 378; DB 5; Length 670;
Best Local Similarity 26.4%; Pred. No. 5.3e-23;
Matches 102; Conservative 79; Mismatches 165; Indels 40; Gaps 10;
QY 7 ANFSCVHESVGLGVYVAVSVGVVAVTGTGVTGNTLLALAIQPKLRTFNLLIA 66
DB 26 ADATGFSQLLTFAAVMT---FLIMVIGCGNLTIVALLKCPKVRNVAATIIISLCIAD 82


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QY 182 LMGIYFVLGLSSVGIFCYLIHROVKRAAQAALQYKLRQASIHNSHNHVARTDEAMPGRFQEL 241
Db 203 LFTAFVPCPLVLIACYAKIFVWVKSEQLKRHATKQNSI-----PNNRLPL 250
QY 242 DSRLASGSPSEGISSEPVSAATTTLEGSDSEVDQINSKRAQMAEKSPPEASAKAQP- 300
Db 251 AS-TGGGALPSGAEQF-----SNRVSSDSSSFSDIVPETAP---SGKQDT 294
QY 301 -IKGARAPDSSEFGKVTMCFVFLCFALSYPFLNLLNILDARVQAPRVVHMLAANT 359
Db 295 RVKDQREVRAKNEW-RITKWLVAIFLSFVVCVLPITIVKVADKNVEHPS-LHICSYILL 352
QY 360 WINGCINPVLVYAMNQFRQAYGSIL 385
Db 353 YLSACINPIIYVIMNKQYKAYKTVV 378

RESULT 7
077269
ID O77269 PRELIMINARY; PRT; 572 AA.
AC O77269;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE EG:22E5.10 protein.
GN EG:22E5.10 OR CG4313.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy L., Harris D., Barrell B.;
RT "Sequencing the distal X chromosome of Drosophila melanogaster.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Benos P.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031765; CAA21124.1; -.
DR PIR; T13740; T13740.
DR FlyBase; FBgn0025632; EG:22E5.10.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPT_F1_2; 1.
DR PROSITE; PS00262; G PROTEIN RECEPT_F1_2; 1.
SQ SEQUENCE 572 AA; 64304 MW; 8E19D28CB61CCD26 CRC64;

Query Match 15.1%; Score 309; DB 5; Length 572;
Best Local Similarity 22.4%; Pred.No. 2.6e-17;
Matches 102; Conservative 83; Mismatches 180; Indels 90; Gaps 10;

QY 9 FSCVHESVLGVRVAVSGVWVAVTGVGNVLTALLAIQPKLRTFRNLLIANLTADLL 68
Db 100 FEGYSDELLTAWAC---IVFIIVGVPGNLITVALSRGRTNSTAIFINLSCDLL 156
QY 69 YCTLQFSDVDTYHLHWRTGATFCRVGGLLFPASNSVILTCILTAIGRYLLIAHPKLF 128
Db 157 FGCNPLAASTKERATWTHSDLLCRLLFPMRLYGLLAVSLLSLTINRYIIAHPROQY 216
QY 129 POFVSAAGIVLALVSTWVGVSAPF---LWPIYILVVPVCTCFDRIR-GRPYITILM 183
Db 217 PRIQRYLLAMVAGTWITFTSIMPTRWGVIPLGLDVSIGCSIMHDYGRSPKEFLF 276
QY 184 GIYFVLGLSSVGIFCYLIHROVKRAA-----QALDQYKLRQ 219
Db 277 IAAFVWPCICIVICYARIFLLVRKAALRAGTAGKTNVSDVTPSSAPQHQIQAVATPKKPE 336

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RESULT 8

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09W533
ID O9W533 PRELIMINARY; PRT; 572 AA.
AC O9W533;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE EG:22E5.10 protein.
GN EG:22E5.10 OR CG4313.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe C., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew K.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Feiraz C., Ferrier S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.F., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";

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QY 220 ASIHNSHNHVARTDEAMPGRFQELDSRLASGGPSEGISSEPVSS----- 260
Db 337 KVTSS--GEANEPIAGRPFFVEENLAYIDNASTDLSPTSYSIRRRDQDQPPVDAV 394
QY 261 -----AATTQLEGSDSEVDQINSKRAQMAEKSPPEA----- 294
Db 395 VLKREKXERDRDQKVSLGRSQTQLEMGKTHGKKNPITTSLTFTFRSPKSHVSMGN 454
QY 295 SAKAQPIKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNLLNILDARVQAPRVH-- 352
Db 455 TSNASSIYFGS-----MSAKDRRLKMLIVFVFWVICYLPITIVAKIWKSAFE----VHWF 506
QY 353 -MLAANLTWLMGCTNPVLVYAMNQFRQAYGSILK 386
Db 507 NIAGVLLIYLTCTINPLIYVLMSEYRAYWNLLR 541

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Science 287:2185-2195(2000).
 RT -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF003422; AAF45710.1; -.
 DR FlyBase; FBGN0025632; EG:22E5.10.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_Rhodpsn.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 572 AA; 64317 MW; 8B19D4E0BE2122C6 CRC64;
 Query Match 15.1%; Score 309; DB 5; Length 572;
 Best Local Similarity 22.4%; Pred. No. 2.6e-17;
 Matches 102; Conservative 83; Mismatches 180; Indels 90; Gaps 10;
 QY 9 FSCYHESVLGYRVAAGVAVTGVNLTLLALAIQPKLRTFRNLLIANLTADLL 68
 DB 100 FEGISDELLTAWAC---IVFIIVGPNLTTVALSRGQRTNSTAIFILNSCSDL 156
 QY 69 YCTLLQPSVDYTLHLHWRGATPCRVFGLLFPASNSVSLTCLIALGRYLLIAHPKLF 128
 DB 157 FGCNLPPLAATFKERAWTHSDLLCLFLPMLRYGLLAVLSVSLITINRYIIAHPRQY 216
 QY 129 POFSAKIGVIALVTSVVGVASPAP---LWPIYILVVPVCTSPDRIR-GRPYTILM 183
 DB 217 PRIYQRYALMVAAGTWTITFSIMPTWVGWGLFGLDVGSCSINHDIYGRSPKEFLF 276
 QY 184 GIYFVLGLSSVGIYCIHLHQRVKA---QALDQYKLRQ 219
 DB 277 IAAFWPCICIVICARIFILVRKAIRAGTAGKTNVSDVTPSSAPQHQAQVATPKKPE 336
 QY 220 ASIHSHVARDAMPGRFQELDSRSLASGPGSEGISSEPV---260
 DB 337 KVTTS--GEANEPIAGRPFVVENLAYIDNASTDSLPIYSIRRDQDQPPVDANV 394
 QY 261 -----AATTQLEGDSSEVGDQINSKRAQMAEKSPPEA-----294
 DB 395 VLKEREKDRDQKVSILGRSQTQLENGKTHKXNPITTSRTTSFTFRSPKSHYASGMN 454
 QY 295 SAKAQPIKAGRAPDSSEFGKVTMCFVFLCFALSYIFLLNLILDARQAPRVVH--352
 DB 455 TSNASSIYPGR---MSAKDRRLKMLTVFVFWFVICYLPITVAKIWKSAE---VHWF 506
 QY 353 -MLAANLTWLGNCINPVLVYAMNRPQRAYGSILK 386
 DB 507 NIAGYLLIYLTTCINPLIYVLMSEYRAYWNJLR 541

RESULT 9
 Q8WPA2 PRELIMINARY; PRT; 361 AA.
 AC Q8WPA2;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Allatostatin receptor BAR.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Lyon 200 BA/Lyon 300 AB;
 RX MEDLINE=21601656; PubMed=11590150;
 RA Secher T., Lenz C., Cazzanali G., Sorensen G., Williamson M.,
 RA Hansen G.N., Svane P., Grimmelikhuijzen C.J.P.;

"Molecular Cloning of a Functional Allatostatin Gut/Brain Receptor and an Allatostatin Preprohormone from the Silkworm Bombyx mori";
 RL J. Biol. Chem. 276:47052-47060(2001).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF303370; AAL47056.1; -.
 DR EMBL; AF303368; AAL47056.1; JOINED.
 DR EMBL; AF303369; AAL47056.1; JOINED.
 DR EMBL; AF254742; AAG44631.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_Rhodpsn.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 361 AA; 40478 MW; 63C2B2846FC3010A CRC64;
 Query Match 14.5%; Score 295.5; DB 5; Length 361;
 Best Local Similarity 22.4%; Pred. No. 1.9e-16;
 Matches 88; Conservative 61; Mismatches 111; Indels 133; Gaps 10;
 QY 20 RVAVSWGUVAVTGVNLTLLALAIQPKLRTFRNLLIANLTADLLYCTLLQPSVD 79
 DB 43 RVYPIFFG-FIGIVGLVGNALVWVAANPGMRSTNLLIINLAVADLLVIFCVPEFTAT 101
 QY 80 TYLHLHWRGATPCRVFGLLFPASNSVSLTCLIALGRYLLIAHPKLFPOVFSAGKIVL 139
 DB 102 DYVWRPWFPGDWCKVQYFIVTAAHSVYTLVMSLDRFMVAVVPTASMSIRTEKALL 161
 QY 140 ALVSTVWVVGVSFAPLWPIYILVPPVC-----TCSPDRIRGRPYTILMGI 185
 DB 162 AIACIWWVILTAIPVG-----ICHGEREYSVFNHNSCVFLEBERGYSKLGQMSF 213
 QY 166 Y---FVLGLSSVGIYCIHLHQRVKAQALDQYKLRQASIHSHVARDAMPGRFQEL 241
 DB 214 FLSSVIFLALISVLYMCL-----233
 QY 242 DSRLASGPGSEGISSEPVSAATTTLEGDSSEVGDQINSKRAQMAEKSPPEASAKAQPI 301
 DB 234 -TELKWSAPGGRVSAE-----SRGRK-----254
 QY 302 KGARAPDSSEFGKVTMCFVFLCFALSYIFLLNLILDA-----RVQAPRVVH 352
 DB 255 -----KVTMVMVVVVVFAVCMWCPICQIILLVKALNKYHITYTFTVTAQIVSH 300
 QY 353 MLAANLTWLGNCINPVLVYAMNRPQRAYGSIL 385
 DB 301 VLA---YVNSCVNPLVYAFVLSNFRVAFKVM 329

RESULT 10
 Q9GK99 PRELIMINARY; PRT; 414 AA.
 AC Q9GK99;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Dopamine D2 receptor short isoform.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20510028; PubMed=11054572;
 RA Myeong H., Jeung D., Kim H., Ha J.H., Lee Y., Kim K.H., Park C.,
 RA Kaang B.;
 RA "Genomic analysis and functional expression of canine dopamine D2


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RT receptor."
RL Gene 257:99-107(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR ENBL, AR293964; AG34497.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 414 AA; 47288 MW; 4E330ADCA0FCB5C CRC64;

Query Match 14.2%; Score 289; DB 6; Length 414;
Best Local Similarity 27.1%; Pred. No. 8.1e-16;
Matches 107; Conservative 68; Mismatches 176; Indels 44; Gaps 14;

QY 19 YRYVAVSGWVAVTGTGNNVLTLLALAIQPKLTRFNLLIANLTLLADLLYCTLLQPPSV 78
DB 34 YNYVAMLLTLLIFII-VFGNVLVCMVAVSREKALQTTNNLVLSLAVADLLVATLVMPVV 92

QY 79 DTVLHL--HWRTGATCRVFGLLLFASNSVILTLCLIALGRYLLIAHKLPPQVFSAG 136
DB 93 --YLEVVGEMKFRIRHCDIFVTLDVMMCTASILNLCASIDRYTAVAMPMLNYTRYSKR 150

QY 137 IVLALVS-TWVGVSFAPLWPIYIIVPVVCTGSPDRIRGRP-----YTTIL-MGYFVLG 190
DB 151 RVTVMTAVVLSFTISCLP-----IFGLNNTDQECIANPAFYVYSIVSYVFFIYT 205

QY 191 LSVGIFYCLIHQVRAAALDOYKLRQASHNSHVARTDAMPGRFOELD-SRLASGG 249
DB 206 LLVYIKIYIVLRRRRRV-----NTRSSRAFRANLKAFLKEA-ARRAQELEMELMSSTS 259

QY 250 PSEGISSEPSVAATTTLEGDSSEVG-----DQINSKEAKQMAEKSPP 293
DB 260 PPERTYSPIPPSSHQHTLPDSHHGLHSTADSPAPKEKNGHAKDHPKIAKIFEQSMEN 319

QY 294 ASAKAQPIKGARRAPDSSEFGVTRMCFVFLCFALSYPILLNILDARVQAPRVAM 353
DB 320 GKRTS-LKTMSSRRLLSQQKEKATQMLAIVLGVFIICWLPPFIITHLNHCBC-NIPPV 377

QY 354 LAANLTLW---NCGINPVLVYAMNRQFRQAYGSIL 385
DB 378 LYSAFTWLGWYNSAVNPPIYTTFNIEFRKAFKLKIL 412

RESULT 11
Q8CGI5 PRELIMINARY; PRT; 459 AA.
AC Q8CGI5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to adrenergic receptor, alpha 1b (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP STRAIN=FVB/N; TISSUE=Liver;
RA Strauberg R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC037002; AAH37002.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
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DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR KW Receptor.
FT NON_TER 459 459
SQ SEQUENCE 459 AA; 50751 MW; C2A7D2EB44816338 CRC64;

Query Match 14.2%; Score 289; DB 11; Length 459;
Best Local Similarity 25.2%; Pred. No. 9.2e-16;
Matches 104; Conservative 74; Mismatches 161; Indels 74; Gaps 15;

QY 2 WNS-SDANFSCYH-----SVLGRYV--AYSGWVVA---VTGTVGNVLTLLALAIQPKL 51
DB 17 WGEIKDANFTGPNQTSNSNLTLPQDVTRAISVGVLGAFILFAIVGNILVLSVACNRHL 76

QY 52 RTRFNLIANLTLLADLLYCTLLQPPSVDTYHLHWRTGATCFRVFGLLFFASNSVSLTL 111
DB 77 RTPNYFIVNLAIDLLLSFTLPFSATLEVLGVWLGRIFCDIWAAVDVLCCTASILSL 136

QY 112 CLIALGRYLLIAHKLPPQVFSAGIVLALVSTVVG-VASFAPL--WPYILVPPVCTC 168
DB 137 CAISIDRYIGVRSLOYPQLVTRKAILALLSVVLSTVISIGLLGKWK-----SPAEND 192

QY 169 SFDIRGRPYTTILMGI-YFVLGLSSVGIFYCLIHQVRAAALDOYKLRQASHNSHV 227
DB 193 KECGVTEEPFVALPSSLSGFYIPLAIVLMVCRVYIVAKRTTKNLEAGVMKEMS----- 246

QY 228 ARTDEAMPGRFOELDSRLASGSPSEGISSEPSVAATTTLEGDSSEVGQDINSKRAQMA 287
DB 247 -----NSKELTLRIHSKNFHE-----DTLSSTKAK--- 271

QY 288 EKSPPEASAKAQTPIKGARRAPDSSEFGVTRMCFVFLCFALSYPILL--LNILDAR 344
DB 272 -GHNPRSSIAVAKLFKFSRE-KKAATLGIIVGM-----FILCWLPEFFIALPLGSLPST 322

QY 345 VQAPRVVMELANLTWLMGNCINPVLVYAMNRQFRQAYGSILK---RGRSPFHR 394
DB 323 LKPPDAVFKVFWLGYFNCLNPIIYPCSSKEFKRAFWRILGQCQCGRRRRR 375

RESULT 12
Q9DBL0 PRELIMINARY; PRT; 515 AA.
AC Q9DBL0
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Adrenergic receptor, alpha 1b.
GN ADRA1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustigich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 403:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AK004891; BAB23647.1; -.
 DR EMBL; AK043877; BAC31691.1; -.
 DR MGD; MGI:104774; Adra1b.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 515 AA; 56497 MW; 69D724E9978F81C1 CRC64;

Query Match 14.2%; Score 289; DB 11; Length 515;
 Best Local Similarity 25.2%; Pred. No. 1.1e-15;
 Matches 104; Conservative 74; Mismatches 161; Indels 74; Gaps 15;
 QY 2 WNS-SDANFSCYH- ----SVLGRIYV--AVSWGIVVA---VTGTGNGVLTLLALAIQPKL 51
 DB 17 WGEKLDANFTGPNQTSNSTLPQLDVTVAISVGLVGLAFILFAIVGNILVLSVACNRHL 76
 QY 52 RTRNLIANTLADLYCYTLQPSVDVTLHLHWRGATFCRVFGLLLFASNSVILTL 111
 DB 77 RPTNYFIVNLAIALDLSFTLVLFATLVGLVWLVGRIFCDIWAADVCLCTASILSL 136
 QY 112 CLIALGRYLLTAHKLPPQVFSAGIVLALVSTWVVG-VASFAPL--WPIYILVPPVVC 168
 DB 137 CAISIDRYIGVRSYQVYPTLVTRKAILALLSVLSTVISIGPLLGK----EPAPND 192
 QY 169 SFDRIQRPTTILMGI-YFVLGLSSVGIFCYLIHQVRAAALDQYKLRQASIHNV 227
 DB 193 KECGVTEEPFALPSSLSGSFYPLAVILVMYCRVYIVAKRTTNLEAGVNMKMS----- 246
 QY 228 ARTDEAMPGRFOELDSLRSAGSGEGISSEFPVSAATTQTLEGDSSEVGDQINSKRA 287
 DB 247 -----NSKETLRIHKNFHE-----DTLSSTKAK--- 271
 QY 288 EKSPPEASAKAQPICKARRAPDSSESSEFGKTRMCFVFLCFALSYIPFL--LNTLDAR 344
 DB 272 -GHNPRSSIAVKLFKFSRE-KKAATLIGIVVGM-----FILCWLPFFIALPLGSLFST 322
 QY 345 VQAPRVVHMLAANLTWLGNCINPVLVYAMNRQFQVAGSTLK---RGPRSFHR 394
 DB 323 LKPPDAVFKVFWLVGYNLNCINPIIYPCSSQEFKAFQNVLRIOQLERRROSSKHAL 356

RESULT 13

Q8BUE5 PRELIMINARY; PRT; 427 AA.
 AC Q8BUE5;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DE Adrenergic receptor.
 GN ADRA1A.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AK085653; BAC39495.1; -.
 DR MGD; MGI:104773; Adra1a.
 DR GO; GO:0008217; P:regulation of blood pressure; IMP.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 427 AA; 47515 MW; 3810E9DSFSA09317 CRC64;

Query Match 14.1%; Score 288.5; DB 11; Length 427;
 Best Local Similarity 23.1%; Pred. No. 9.2e-16;
 Matches 97; Conservative 78; Mismatches 148; Indels 97; Gaps 14;
 QY 3 NSSDANFSCYHESVLGRIYVAVSWGIVVA---VTGTGNGVLTLLALAIQPKLRFNLLI 59
 DB 7 NASEGS-NCTHPPAQVNTSKAILLGVILGLLIIFGVGLNVLVLSVACHRHLSVTHYI 65
 QY 60 ANLTADLYCYTLQPSVDVTLHLHWRGATFCRVFGLLLFASNSVILTLCLIALGRY 119
 DB 56 VNLVADLILSTVLPPSAIFEILGYWAFGRVFNINAVDVLCCTASIMGLCIISIDRY 125
 QY 120 LLIHAKPLFPQVFSAGIVLALVSTWVVG-VASFAPLWPIYILVP---VWTCSEFDIRG 175
 DB 136 IGVSYPYRPTVITQRRGVALLCWALSLVISIGPLFGWRQQAPEDETIC-----QINE 180
 QY 176 RPYTILMGI-YFVLGLSSVGIFCYLIHQVRAAAL-----DQYKLRQASIH 223
 DB 181 BGVYVLFALSGFYVPLTILVMYCRVYIVAKRESGLKSLKTDKSDSEQVTLR---IH 237
 QY 224 SNHARTDEAMPGRFOELDSLRSAGSGEGISSEFPVSAATTQTLEGDSSEVGDQINSKRA 283
 DB 238 RKNV-----PAEG---SGVSSAKNKT-----HFSVRL 262
 QY 284 KOMAEKSPPEASAKAQPICKARRAPDSSESSEFGKTRMCFVFLCFALSYIPFL--LNTILDA 343
 DB 263 KFSREK-----KAAKTIGIVVGVFCVLCWLPFFLWVPIGS 296
 QY 344 --VQAPRVVHMLAANLTWLGNCINPVLVYAMNRQFQVAGSI-----LKRGRSFHR 395
 DB 297 PFPNFKPPTVFKIVFWLVGYNLNCINPIIYPCSSQEFKAFQNVLRIOQLERRROSSKHAL 356

RESULT 14

Q8BV77 PRELIMINARY; PRT; 466 AA.
 AC Q8BV77;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DE Adrenergic receptor.
 GN ADRA1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=22354683; PubMed=12466851;

